GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd. Copyright

OM protein - protein search, using sw model

Search time 59 Seconds (without alignments) 4635,127 Million cell updates/sec August 25, 2004, 17:06:26; Run on:

US-09-442-489F-2 14575 1 MAAASYDQLLKQVEALKMEN.......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 seqs, 96191526 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

summaries Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 su

Database :

PIR 78:*

1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

1		ф (
No.	Score	Query Match	Length	DB	ID	Description
1	145	9.7	284	-	BHUA	adenomatous polypo
N	13148	90.2	2845	N	95	adenomatous polypo
m	œ	24.1	27	7	3025	adenomatous polypo
4	778	ď.	41	0	1382	
'n	œ	٠	32	7	56	microtubule-associ
9	518		27	C/	9007	hypothetical prote
7	517		23	~	4	hypothetical prote
œ	516.5		18	N	2332	щ
σ	14		18	C)	333	
10	477		77	N	35	microtubule-associ
11	452		50	7	4	hypothetical prote
12	442		77	~	20	cell wall surface
13	ന	2.9	72	N	0	hypothetical prote
14	426.5		73	N	32	protein F07All.6 [
72	OD.		79	(7)	34	hypothetical prote
16	417		68	N	47	alpha-A-crystallin
17	4		93	N		cell proliferation
18	412.5		48	N	T34418	hypothetical prote
19	410		18	N	α	nascent polypeptid
50	409	٠	52	N	~	hypothetical prote
21	406		17	N	534	hypothetical prote
22	405		94	N	273	Bassoon protein -
23	396	2.7	71	7	89	hypothetical prote
24	395		92	N	43	ankyrin 2, neurona
25	392.5		14	7	96	hypothetical prote
26	391		20	C)	265	hypothetical prote
27	387.5		18	7	583	364K Golgi complex
28	384	2.6	45	۲3	T32271	hypothetical prote
29	382.5	5.6	17	7	380	toucan gene protei

microtubule-associ ankyrin 3, long sp profilaggrin - hum chondroitin sulfat trithorax homolog hypothetical prote cell proliferation nuclear/mitotic ap hypothetical prote microtubule-associ nuclear receptor c Tpr homolog - frui peroxisome prolife	erythrocyte membra	cell proliferation
A56577 A55575 A31938 A41931 A44265 T119431 T30336 T730336 T73035 T13023	A46203 D71623	B48666
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332542 33252 325	2441	2897
	2 6	2.5
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KESULT 1 RAHITAP
adenomatous polyposis coli protein - human
N; Alternate names: polyposis coli locus protein DP2.5; tumor suppressor APC
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1991 #sequence revision 31-Dec-1991 #text_change 21-Jul-2000
C;Accession: A37261; B39658; A44928; A49319; I54271
R;Kinzler, K.W.; Nilbert, M.C.; Su, L.K.; Voqelstein, B.; Bryan, T.M.; Levy, D.B.; Smith,
chul, S.F.; Horii, A.; Ando, H.; Miyoshi, Y.; Miki, Y.; Nishisho, I.; Nakamura, Y.
Science 253, 661-665, 1991
A; Title: Identification of FAP locus genes from chromosome 5q21.
A; Reference number: A37261, MUID: 91335210, PMID: 1651562
A; Accession: A37261
A; Molecule type: mRNA
A;Residues: 1-2843 <kin></kin>
A; Cross-references: GB: M74088; NID: g182396; PIDN: AAA03586.1; PID: g182397
R;Joslyn, G.; Carlson, M.; Thliveris, A.; Albertsen, H.; Gelbert, L.; Samowitz, W.; Grode
arrington, J.; McPherson, J.; Wasmuth, J.; Le Paslier, D.; Abderrahim, H.; Cohen, D.; Ler
Cell 66, 601-613, 1991
A; Title: Identification of deletion mutations and three new genes at the familial polypos
A; Reference number: A39658; MUID: 91330307; PMID: 1678319
A;Accession: B39658
A. Wolonia time. DNA

A, Molecule type: DNA
A, Rolecule type: DNA
A, Cross-references: GB:M73446; NID:9190163; PIDN:AAA60354.1; PID:9190164
A, Cross-references: GB:M73446; NID:9190163; PIDN:AAA60354.1; PID:9190164
CA, Reference number: A445, 1929
A, Title: Disruption of the APC gene by a retrotransposal insertion of L1 sequence in a cc
A, Reference number: A44928; MUID:92119623; PMID:1310068
A, Molecule type: DNA
A, Rocession: A44928
A, Molecule type: DNA
A, Rolecule type: MANA
A,

C,Genetic A,Gene: G A,Cross-r	s: 1DB:APC eferences: GDB:119682; OMIM:175100	8 8	SHRSKQRHKQSLYGDYVPDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSS RRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVS
A; Map pos A; Note: m C; Superfa C; Keyword F; 1-730/D	A; Map position: 5q21-5q22 A; Note: mutations of this gene can result in familial adenomatous polyposis or sporadic C; Superfamily: adenomatous polyposis coli protein C; Superfamily: adenomatous polyposis coli protein C; Keywords: cancer; familial adenomatous polyposis; tumor suppressor F; 1-730(Domain: leucine-rich ARTD) F; 1-730(Domain: leucine-rich ARTD)	6 6 6	LDSSRSEKDRSLERERGIGLGLANTHPATENPGTSSKRGLOISTTAAQIAKVWEEVSAIHTIS 90 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNITVNFTKSENSNRTCSMPYAKLEYKRSS 96 [[[[[[[[[]]]]]]]][[[[[[]]]]]]][[[[[]]]]]
F;185-227 F;731-283 F;1131-11 F;1558-15 F;1866-18	yelon: coll #status predicted 12/Domain: serine-rich <ctd> 156/Region: acidic 1577/Region: acidic</ctd>	3 & 8	QEARSSOSITELECVIEDENCALENCES SANTIGENIN INCENTALICAL INCELLANCE OF THE SANTIGENING OF T
Query M Best Loo Matches	. Match 15 Milarity 99.7%; Score 14533; DB 1; Length 2843; Local Similarity 99.8%; Pred. No. 0; Os 10 September 1; Mismatches 5; Indels 0; Gaps 0;	상 입	LDTPINYSLKYSDEQLINSGRQSPSONERWARPKHIIEDEIKQSEQRQSRNGSTTYPVYTE 108
& g	1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 60 	දු දු	STUDANTAR VERRAQUECVS TREADMINISTERIA VOSANGERIA VA VA SALA VA
දු දු	61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKASLRSYGSREGSVSSRSGECSPVPMGSFPR 120 	දි දි	TNYSERYSEEEQHEEERPTYYSIKYNEEKHYDQPIDYSLKATDIPSSQKQSF8FSKS 120
oy Dp	121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180 	& 4a	SSGQSSKTERMSSSSENTSTPSSNAKRONOLHPSSAQSRSGOPQKAATCKVSSINOFT10 126
\$ 95 05	OTDLIRROLEYBARQIRVAMBEQLGTCODMEKBAQRRIARIQOIEKDILRIROLLQSQAT :	දු දු	TYCVEDPICESRCSSLSSAEDBIGCNQTTQEADSANTLQIABIKGKIGTRSAEDPV 132
\ \ \	EARERSONKHETGSHDAERQNEGGGGGEINWATSGNGGGSTTRWDHETASVLSSSSTHSA FARRSONKHETGSHDAERQNEGGGGGGEINWATSGNGGGSTTRWDHETASVLSSSSTHSA FARRSONKHETGSHDAERQNEGGGGGGG	දුරු දුර	1321 SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQFT 1380 1321 SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPHYVQFT 1380
i 6 f	PRRITEHIGENCE CONTINUED TO THE PROPERTY OF THE PROPERTY OF THE PRESENCE OF THE PROPERTY OF THE	& A	1381 PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPP 1440 1381 PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPP 1440
1 & 1	HONDKOSVLLGNSRGSKEARARASAALHNIIHSOPDDKRGREIRVLHLLEQIRAYCETC 42	& 8	1441 PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHPATESTPDGF 1500
3 & 6	HENDALDS ULGSNORGSKEARTHEADALDEN ITRSQPORKSKREIRVURLLEEGIRAITEIC 12 WEWQEAHEPGMDODKOPMPAPPEHOICPAVCVIMKLSFDEERRHAMNELGGLOAIAELLO 48 WEWQPAHEPGMOOKNOWED DIVERCILLE	ry da	1501 SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNBTESEQPKESNENQEKBAEKTIDSE 1560
3	VDCEMYCLINDHYSITLERYAGMALTNIFFGDVANKATLCSMKGCMRALVAQLKSESDL	& 8	1561 KDLLDDSDDDDIEILEECIISAMPTKSSRKCKKPAQTASKLPPPVARKPSQLPVYKLLPS 1620
3 8 8	01 VOCERT CELLINDIAS I LEGINALINE ESTANDAMENTE CONTROCCIONAL VAÇENSES ESTED SE 41 QOVIASVLRILGHRADVINSKRILREVGSVKALMECALEVKKESTIKSVLSALMINISAHCT 60 61 OOVIASVL PINISCHE SINISKRILDEVICSVRALMICKAL FVKEPSTIKSVL SALGALISH FILL	ò a	1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680
3 8 1	GX 1555 CLANDS READ VACANTIBES VGS SATERICADE SALES TELS VEDALERANDES EN VEDAL	oy Db	1681 SGEFEKRDTIPPEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP 1740
8 8 8	601 ENKADICAVDGALAFLVGILITRKSQINTLAIIESGGGILENNYSSLIAINEDHRQILKENN 660 661 CLOTLLOHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDMGAVSMLKNLIHSKHKMIAM 720 661 CLOTLLOHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDMGAVSMLKNLIHSKHKMIAM 720 661 CLOTLLOHLKSHSTTIVSNACGTLWNLENNYSTANGANISWLKNLIHSKHKMIAM 720	65 da	1741 FRVKKIMDQVQQASASSAFNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNIN 1800
3 8 1	GEAL PLENT CONTROL OF THE CONTROL OF	oy G	1801 AERVESDNKDSKKONLKANSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860
dy Qy	721 GSAAALKNIMENKRAXXKUNAIMSPGSSLEPILHVKKKKALEAELIJAKHIBEIFUNIUNIS 780 781 PKASHRSKQBHKQSLYGDYVPDINEHDDNRSDNRNTGNATVLSPYLNTTVVLPSSSSRGS 840 	Qy Db	1861 SLSSLDFDDDDVDLSREKAEIRKAKENKESEAKVTSHTELTSNQOSANKTQAIAKQPINR 1920

118-09-442-4891-2.rDr

of the

RESULT 2
149505
adenomatous polyposis coli protein - mouse
N;Alternate names: APC
C;Species: Mus musculus (house mouse)
C;Date: O2-Jul-1996 #sequence_revision 02-Jul-1996
C;Accession: 149505

#text_change 13-Aug-1999

homolog 10; LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS OTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT WEWQEAHEPGMJQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT CLOTILIQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDMGAVSWLKNLIHSKHKMIAM CLQTLLQHLKSHSLTIVSNACGTLWNLSARNFKDQBALWDWGAVSMLKNLIHSKHKMLAM GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS PKASHRSKORHKOSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGS EAERSSONKHETGSHDAERONEGOGVGEINWATSGNGOGSTTRWDHETASVLSSSSTHSA PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLFLLIQLL PRRLITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL HGNDKDSVLLGNSRGSKEARARARALHNI IHSQPDDKRGRREIRVLHLLBQIRAYCETC RGFVNGSRESTGYLEELEKERSLILLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM Gaps murine PID:9191992 2845; the R;Su, L.
Science S56, 668-670, 1992
Science S156, 668-670, 1992
A;Title: Multiple intestinal neoplasia caused by a mutation in A;Reference number: 149505; MUID:92263101; PMID:1350108
A;Accession: 149505
A;Actaus: preliminary; translated from GB/EMBL/DDBJ
A;Rolecule type: mRNA
A;Residues: 1-2845 RES>
A;Cross-references: GB:M88127; NID:91991; PIDN:AABS9632.1; PI
C;Superfamily: adenomatous polyposis coli protein Length Indels 159; DB s; Score 13148; s; Pred. No. 0; 113; Mismatches Query Match 90.2%; Best Local Similarity 90.0%; Matches 2566; Conservative 11. 8 6 8 6 6 B 6 원 장 원 \$ B \$ 원 수 명 8 6 6 6 8 8 8 음 성 음 8 8 8

	RSEKDRSLERERGIGLSAYHPTTENAGTSSKRGLQITTTAAQIAKVMEEVSAIHTS SSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS	Oy 1979 -MNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD 2037	
on on		1977 NNNKESEPIKEAEPANSGGEPSKPQASGYAPKSFHVEDTPVCFSRNSLSSLSIDSEDD 203	
961	1 NDSLNSVSSNDGYGKRGGWKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE 1020 	2038 LLOECISS 2037 LLOECISS	
102	1 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSTUVPVYTE	Qy 2098 NFDWRAIQEGANSIUSSLHQ-AAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEE 2156 	
108	STDDKHLKRQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQBDDYEDDXP 11	Qy 2157 KPFTSNKGPRILKPGEKSTLETKKIESESKGIKGCKKVVKSLITGKVRSNSEISGQMKQP 2216	
114	TINYSERYSEEDQH-EEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSK 119	OY 2217 LOANMPSISRGRTMIHIPGVRNSSSTSPVSKKQPPLKTPASKSPSBGQTATTSPRGAKP 2276	
120	SSGQSSKTEHMSSSENTSTPSSNAKRONOLHPSSAQSRSGOPOKAATCKVSSINOETI 125	OY 2277 SVKSELSPVARQTSQLGGSSKAPSRSGSRDSTPSRPAQOPLSRPIQSPGRNSISPGRNGI 2336 2277 AGKSELSPITRQTSQLSGSNKGSSRSGSRDSTPSRPTQQPLSRPMQSPGRNSISPGRNGI 2336	
126	SKIGTRSAEDP 13 SNDVTRSAEDP 13	QY 2337 SPPNKLSQLPRTSSPSTASTKSSGGGKMSYTSPCRQMSQQNLTKQTGLSKNASSIPRSES 2396	
132	O VSEVPAVSQHPRIKSSRLQGSSLSSESARH-KAVEFPSGAKGPSKGGAQTPKSPEHYVO 13	OY 2397 ASKGLNOMNNGANKKVELSRMSSTKSSGSESDRSERPULVRÖSTFIKEAPSFILRRKL 2456	
137	9 ETPLMFSRCTSVSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGGTMPPSRSKT 14	OY 2457 EESASFESLSPSSRPASPTRSQACTPVLSPSLPDMSLSTHSSVQAGGMRKLPPNLSPTIE 2516	
143	9 PPPPPQTAQTKREVPKOKKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPD 149 	CY 2517 YNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLERVSTWRRTGSSSSILSA 2576	
149	9 GFSCSSSLSALSLDEPFIQXDVELRIMPPVQENDNGNETESEQPKESNENOEKEAEKTID 155	QY 2577 SSESSEXAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEPSFINGTSQTVSSGAIN 2636	
വ വ	9 SEKDLIDDSDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLEPPVARKPSOLPVYKLL 161	Oy 2637 GAESKTLIYOMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKD 2696	
161	P PSQNRLQPQXHVSFTPGDDMPRVYCVBGTPINFSTATSLSDLTIESPPNBLAAGEGVRGG 167	OY 2697 SKDNQAKONVGNGSVPMRITVGLENKLISFIQVDAPDQKGTEIKPGONNPVPVSETNE 2753 : : :	
167	A QSGEFEKRDII PTEGRSTDEAQGGKTSSVTIPELDDIKAEEGDILAECINSAMPKGKSH 173:	Qy 2754 SPIVERTPPSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNT 2813 :	
173	9 KPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNN 1791	Qy 2814 KKRDSKIDSTESSGTQSPKPHSGSYLVTSV 2843	
179	NSKDFNDKLPNNEDRVRGSFAFDSPHYTPIEGTPYCFSR 18 :	RESULT 3 T30258 adenomatous polyposis coli protein 2 - mouse	
1859	AKENKESEAKVTSHTELTSNQQSANKTQALAKQPI 19 : : : : : :) on 22-0	
1919	NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQE 1977	Ryvan Es, J.H.; Kirkpatrick, C.; van de Wetering, M.; Molenaar, M.; Miles, A.; Kuipers, Curr. Biol. 9, 105-108, 1999 A;Title: Identification of APC2, a homologue of the adenomatous polyposis coli tumour sur	., 14
r T	MANGAR, V LÇRÇKI I. FÇGGALUĞFURGAA I DEALIÇNLA I ENTEVCIFSKNISI LIŞBI DIÇ	7086; PMID:10021369	

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6 6 6 6 6 6	6 6 6 6 6	3 6 6 6 6	1 & 8 & 8 & 1		6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6
A;Accession: T30258 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Molecule type: DNA A;Residues: 1-2274 <van> A;Cross-references: EMBL:AJ130783; NID:g4210431; PIDN:CAA10207.1; PID:g4210432 A;Cross-references: EMBL:AJ130783; NID:g4210431; PIDN:CAA10207.1; PID:g4210432 C;Genetics: A;Gene: APC2 A;Introns: 47/3; 78/1; 138/2; 174/3; 212/3; 238/3; 271/3; 396/1; 428/1; 474/3; 500/3; 53 Query Match Best Local Similarity 34.4%; Pred. No. 1.7e-136; Best Local Similarity 34.4%; Pred. No. 1.7e-136; Matches 1005; Conservative 356; Mismatches 789; Indels 773; Gaps 98;</van>	Qy 4 ASYDOLLKQVEALKMENSNIRQELEDNSNHILTKLETEASNMKEVLKQLGGSIEDEAMA 61	QY 181 QTDLTRRQLEYEARQIRVAMBEQLGTCQDMEKBAQRRIARIQQIEKDILRIRQ 233 178 QMDLIRQQLEFEAQHIRSLWEERFGTSDEWVQRAQIRASRLEQIDKELLEAQDRVQQTEP 237 QY 234LLQSQATEAERSSQNKHFTGSHDAERQNEGGGVGEINMATSGNGQGSTTRMDHFTASV 291 Db 238 QALLAVKPVAVEEEQBAEVPTHPEDGTPQPGN	Db 270	529 529 487 589 589	OY 649 DEDROILEMENT CONTLOCATE CONTLOCATE AND CONTROL OF CONTROL O

PID:g1800229; PIDN:AAB41404.1

nce number: Z17782, MUID:97144426, PMID:8990193 ton: T13825 : preliminary; translated from GB/EMBL/DDBJ

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qq	;	A;Refere	nce number: Z17782; MUID:97144426; PMID:
	EDDLLOECI 2	A;Status A;Molecu	: preliminary; translated from GB/EMBL/DI
		A; Kesidu A; Cross	es: 1-2416 <hay> references: EMBL:U77947; NID:g1800228; P: re:</hay>
	2044 SSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSE-HGLS 2093	A;Gene: A;Cross- A;Map po	A;Gene: D.APC A;Cross-references: FlyBase:FBgn0015589 A;Map position: 3R
	2094 PDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLT 2151 ::: :	Query Match Best Local Matches 72	Match 12.2%; Score 1778.5; ocal Similarity 25.5%; Pred. No. 2.8e-6721; Conservative 330; Mismatches
	2152 PDQEEKPFTSNKGPRILKPGEKSTLETKKI-ESESKGIKGCKKVYKKLITGKVR-SNSEI 2209	ò	GSHDAERON-EG
qq	1703PSKLRKGRKPAAEAGGAWRPEKRGTTSTKINGSPRLPNGPE 1743	qq	: : : : : : : : : :
oy Ob	2210 SGQMKQPLQANMPSISRGRTWIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATT 2269 1744 KAKGTQKAMAGESTMLRGRTVIYSAGPASRTQSKG-ISGPCTTPKKTGTSGTT 1795	දු දු	296 STHSAPRRLTSHLGTKN
δ'n	2270 SPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSI 2329	È	
qq	1796 QPETVTKAPSFEQQRSRSLHRPGKISELAALRHPPRSAT 1834	qq	249 SGNAQSCATLRRSGCMPLLVQMWHAPDND
Qy Db	2330 SPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKWSYTSPGRQWSQQNLTK 2380	දු දු	398 KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGM-
95 Pp 95	2381 QTGLSKNASSIPRSESASKGLNQMNNGNA-NKKVELSRMSSTK 2423	ζζ Op	456 LSFDEBHRHANNELGGLQAIAELLQVDCEMYG-L1
Qy	2424 SSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPV 2483 	y O	515 NKATLCSMKGCMRALVAQLKSBSBDLQQVIASVLR
Qy Db	2484 LSPSLPDMSLSTHSSYQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLP 2540 1	oy da	575 CALEVKKESTLKSVLSALMNLSAHCTENKADICAV
	2541 INRSGTWKREHSKHSSSLERVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGT 2598 	ç da	635 GGGILRNVSSLIATNEDHRQILRENNCLGTLLQHI
	2599 KQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAESKTLIYQMAPAV 2651 :	S G	695 QEALWDMGAVSMLKNLIHSKHKNIAMGSAAALRNI
	2652 SKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNG 2709 2154 RKTSDAVVQTEDVATSKTNSSTSPSLESRDPPQAPA 2189	SP QS	750 PSLHVRKQKALEAELDAQHISETPDNIDNLSPKAS : 650 PILEARKAKALQQELGERHTAETCDNLD
	2710 SVEWRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPFSSSSSK 2769 2190 SGPVAPQGSDVDGPVLTKPPASAPFPHEGLSAVIAGFPTSR 2230	λς q	810 RSDNPNTGNMTVLSPYLNTTVLPSSSSSRGSLDSS
	2770 HSSESGTVAARVIPENKNPSPRKSSADSTSARPSQIPTPVN 2810	ò	870 PGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDR
	2231 HGSPSRAARVPPFNYVPSPMAAATMASDSAVEKAPVSSPAS 2271	Ор	APR
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tch 12.2%; Score 1778.5; DB 2; Length 2416; al Similarity 25.5%; Pred. No. 2.8e-65; 721; Conservative 330; Mismatches 845; Indels 935; Gaps 101; 188 DESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERW 1049 1050 ARPKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANG 1109 397 298 455 514 409 469 STHSAPR------RLTSH-----LGTKVEMVYSLLSMLGTHDKDDMSRTLLLAM 337 574 589 749 649 634 529 694 PSLHVRKOKALEAELDAQHLSETFDNIDNLSPKASHRSKORHKQSLYGDYVFDTNRHDDN 809 677 869 695 734 749 243 ERSSQNKHETGSHDAERQN-EGQGVGEINMATSGNGQGSTTR-----MDHETASVLSSS | :| : | : | : | : ELREWREHRSLDRNFERQSAQQQQLDELPPRNGGSPASAGRPSRSKEPSYTLSRFLDGD 299 KAGRREAKVLRLLDQIVDYCSFLKTLLQSGGEAIADDSDRHPL------AAISSLMK 410 NYALLCGQKQFMEALVAQLDSAPDDLLQVTASVLRNLSWRADSNMKAVLNEIGTVTALAL SSSQDSCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDD KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGM--DQDKNPMPAPVEHQICPAVCVLMK 456 LSFDEEHRHAMNELGGLQALAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA 515 NKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALME 575 CALEVKKESTLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIES 530 AGGILKNVSSHIAVCEPYRQILKQHNCLAILLQQLKSESLTVVSNSCGTLWNLSARSAED 930 THSNTYNFTKSENSNRTCSMPYAKLEYRRSSNDSLNSVSSNDGYGKRGQMKPSIESYSED RSDNFNTGNMTVLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATEN -----KLDKERASSSRRHP----870 PGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAH 635 GGGILRNVSSLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKD QEALWDMGAVSWLKNLIHSKHKWIAMGSAAALRNLMANRPAKYK----DANIMSPG-SSL PTLEARKAKALQQELGERHTAETCDNLD------AHR-----KVKPKITDFDLE | : | | : | | : | | : | | : | | : | | | : | | | : | | | | : | | | : | | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | -----TGG-----ME---129 296 338 398 695 750 650 678 735 cal 8 % B à 8

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T13825 T13825 T13825 C;Species: Drosophila melanogaster C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000 C;Accession: T13825 R;Haysshi, S:;Rubinfeld, B:;Souza, B:;Polakis, P.; Wieschaus, E.; Levine, A.J. Proc. Natl. Acad. Sci. U.S.A. 94, 242-247, 1997 A;Title: A Drosophila homolog of the tumor suppressor gene adenomatous polyposis coli

දුරු දුරු	1996 QGE 1692 VSE	PPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLOECISSAMPKKKK 2052
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6 % 6 %	8N 6 	IVSSIHQAAAAACLSRQASSDSDSILSLKSGI-SLGSPPHLTP 2152 ::: : : TWIAFEARALAENILQPAATDDDTTEMTFSLNSLDLDNIRPPSGMBSLNSCYQDHSQP 1849
ò	3 00	EBKPFTSNKGPRILKPGBKSTLETKKIBSBSKGIKGGKKVYKSLITGKVRSNSEISGQ 2212
qq	1850 SSI	LRQAMPS-KSPRFARKMFPANLVARRALGHLAGSAESVNSSCNLLDN 1897
à i	213 MK	P2ANMPSISRGRIMIHIPGVRNSSSTSPVSKKGPPL2
a è	1898 IKP	PSEMDELDUSMISVUSIQUETANDUSQUENTIINSVSNIETAACUDUIMIN DASCED 193
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ò	2288 OT	SQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPI 2321
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ري در	2344 QL	PRISSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESA 2397
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ò	2444 IK	KEAPSPTLRRKLBESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGG 2503
qq	: : 2231 VKD	
δλ	2504 WRKL	PPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGT"
Db	2259 -S.	KLPTKKGTASGGSPSKAGSPKRIPLAPARRMTPQRANTSIRLAA 2303
ά	564	IGSSSILSASEBSSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFS 262
d d	2304 GKS	paasrvysgrvssttppsrsnsningssaaaaakinqaqsrianiwkrvdeaktik 236
λŏ	2622 PT:	9
Dp	2364 QS	SSSNLRİQKTKSSNMLNANGTKPTLLRSSTFD 2397
δý	2679 TP	PVIDSVSEK 2689
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RESULT 5 T13564 microtubule Microtubule C.5Decies: C.5Decies: C.7Accession C.7Acces	ile-asso tte name s: Droso 3-Aug-1 on: Ti3 to The I to the stion: S	ile-associated protein homolog - fruit fly (Drosophila melanogaster) ter names: hypothetical protein EG:49E4.1 [1.0] 13. Drosophila melanogaster [1.0] 13. Aug-1999 #sequence_revision 13. Aug-1999 #text_change 17.Nov-2000 [1.0] 10.1 Till 19564 [1.0] 10.2 Papagiannakis, G.; Siden-Kiamos, I.; Louis, C. [1.0] 11 to the EMBL Data Library, April 1999 [1.0] 12 to the EMBL Data Library, April 1999 [1.0] 13 to the EMBL Data Library, April 1999 [1.0] 14 to the EMBL Data Library, April 1999 [1.0] 15 to the EMBL Data Library, April 1999 [1.0] 16 to the EMBL Data Library, April 1999 [1.0] 17 to the EMBL Data Library, April 1999 [1.0] 18 to the EMBL Data Library, April 1999 [1.0] 19 to the EMBL Data Library, April 1999 [1.0] 19 to the EMBL Data Library, April 1999 [1.0] 10 to the EMBL Data Library, April 1999 [1.0] 10 to the EMBL Data Library, April 1999 [1.0] 11 to the EMBL Data Library, April 1999 [1.0] 11 to the EMBL Data Library, April 1999 [1.0] 11 to the EMBL Data Library, April 1999 [1.0] 11 to the EMBL Data Library, April 1999 [1.0] 12 to the EMBL Data Library, April 1999 [1.0] 13 to the EMBL Data Library, April 1999 [1.0] 14 to the EMBL Data Library, April 1999 [1.0] 15 to the EMBL Data Library, April 1999 [1.0] 16 to the EMBL Data Library, April 1999 [1.0] 17 to the EMBL Data Library, April 1999 [1.0] 18 to the EMBL Data Library, April 1999 [1.0]

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	1567	AESAKPPIEFREVSRPESVIDGIKDESARPESRRDSPLASKE 1608
	836	SSRGSLDSSRSEXDRSLERERGIGLGNYHPATENPGTSSKRG
_	1609	
	889	KWMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCS 948
	1665	
	949	
	1711	RPASVAESAKDGADDLKELSRPEŠTTQSKEAGSIKDEKSPLASEEAŠRPAŠVAESVKDEA 1770
	1006	HKIHSANHMDDGRQEEDTPINYSLKYSDBQLNSGRQSPSQNERW 1049
	1771	EKSKEESRRESVAEKSPLPSKEASRPASV)
	1050	
	1831	SRPASVAESIKDEAEKŠKEESRRESVAEKSPLPSKEASRPASVAEŠIKDEAEKSKEE-SR 1889
	1096	QECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSE 1145
	1146	120
	1950	: : : :
	1205	SSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVS 1252
	2002	ESVAEKSPLPSKEASRPASVAESIKDE
	1253	SINQETIQTYCVEDTPICFSRCSSLSSLS-SAEDEIGCNQTTQEADS-ANTLQI 1304
_	2062	IKDEAEKSKEESRRESAAEKSPESKEASRPASVAESVKDEADKSKEESRRESMAESGKA 2121
	1305	DC
	2122	QSİKGDQSPLKEVSRPRSVAESVKDDPVKSKEPSRRRSVAGSVTADSARDD 2172
	1358	AKSPSKS-GAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSG 1416
	2173	-OSPLESKGASRPESVVDSVKDEAEKQESRRESKTES 2208
	1417	VPKN-KA
	2209	VIPPKAKDDKSPKEVLOPVSMTETIREDADOPMKPSQAESRRESIAESIKASSPRDEKSP 2268
	1459	TABKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLS 1507
	2269	LASKEASRPGSVAESIKYDLDKPQIIKDDKSTEHSRRESLEDKSAVTSEKSVSRPLSVAS 2328
	1508	1512
	2329	DHEAAVAIEDDAKSSISPKDKSRPGFVAETVSSPIEEATMEFSKIEVVEKSSLALSLQGG 2388
	1513	
	2389	SGGKLQTDSSPVDVAEGDFSHAVASVSTVTPTLTKPAELAQIGAAKTVSSPLDEALRTPS 2448
	1528	VQENDNGNETESEQPKESNENQEKEAEKTIDSEKDLLDDSDDDDIEILEECIISAMPTKS 1587
	2449	APEHISRADSPAECASEEIASÕDKSPQVLKESSRPAMVAESKDDAAQLKSSVEDLRSPVA 2508
	1588	SRKGKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSF 1632
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	2569	TEGDDMFKVICVEGIFINESTAINSESDLILESFFNELAAGEGVRGGAGGEFEAKN 1988 OPAELSKVDTEKTASSTIDESPKSLIGSPAERRYESPAESAKDAAESVEKKKAA 2622
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oda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch, M.; Ohta, T.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; F.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; F.; 357, 1225-1240, 2001
le: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
rence number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                           3625 SKEASR-PTS----VAESVKDEADKSKEESR--------RESGAEKSPLASME 3664
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                                             2728 VDAPDOKGTEIKPGONNPVPVSETNESPIVERTPFSSSSSKHSSPSGTVAARVTPFNYN 2787
                                                                                                                                                                                                                                                                                                  3665 ASRPISVAESVK--DETEKSKEESRRESVIEKSPLPSKEASRPISVAESVKDEAEK-SKE 3721
2615 IKEN-----EFSPTNSTSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPIN 2667
                                                                                                                                     2668 NPRSGRSPIGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLISFIQ 2727
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ss-references: GNS-BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149
srimental source: strain N315
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                letical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
ies: Staphylococcus aureus
:: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
ssion: F90073
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Local Similarity 19.5%; Pred. No. 1.8e-13;
hes 452; Conservative 333; Mismatches 1000; Indels 534; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           --MSMHHTHST 2189
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ULT 7.434 control MOGA9.1a - Caenorhabditis elegans othetical protein KOGA9.1a - Caenorhabditis elegans pecies: Caenorhabditis elegans ate: 29-Oct-1999 #text_change 18-Feb-2000 cession: T34434
                                                                                                                                                                                                                                                                                                                             1746 SLRKSESVS-----ESSSLSGSQSM--SDSVSTSDSSSLSVSTS---LRSSESVSE
                                                                                                                                                                                                                                                                                                                                                                                                2262 SEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1948 STSLSDSISGS-----TSVSDSSSTSTSTSDSMSQSQSTSTSASGSLSTSTSTSSMSM
   2085 RPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISL
                                                                                                                                                                                                                                                           2202 KVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2322 QSPGRNSIS-PGRNGISPPNKLSQLPRISSPSTASTKSSGSGKMSYTSPGRQMSQQNLTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2381 QTGLSKNASSIPRSESASKGLNQMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2441 STFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPS-LPDMSLSTHSSV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2560 RVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2074 -STSTSISESLSTSGSGSTSVSDSTSMSESDSTSVSMSQD---KSDSTSISDSESVSTST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2677 GNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGT
                                                                                                                                    GSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKS---LITG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2002 SASTSSSQSTSVSTSLSTSD-----SISDSTS---ISISGSQSTVESESTSDST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2620 FSPINSTSQTVS---SGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ---TSESIST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2048 SIS-----STSGLSTSDSDSTSTSTSD-----STSG---
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mitted to the EMBL Data Library, December 1996
escription: The sequence of C. elegans cosmid K06A9.
eference number: Z21525
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2115 LHQAAAAACLSRQASSDSDSILSLKGGISLGSPFHLT	DD 1227 TSDGSIVITGSIEGSSISGSSSAISLSSSSFVFSISGSFNFSISGSSIFIFNFSQSIS 1284 Qy 2158 PFTSNK	OY 2192KKVYKSLITGKVRSN-SELSGQMKQPLQANMPSISRGRTMIHIPGVR 2237	2238 NSSSSTSPVSKKGPPLKTPASKSPSEGQIATISPRGAKPSVKSELSPVARQIGGSSK	Qy 2298APSREGSRDSTPSRPAQQPLSRPIQSPGRNSIS-PGRNGISPPNKLSQLP 2346 Db 1445 HTTMSKASSGSTSPSTNSQTGSTVTMGSSSTSGVSTSSASSTQPQMSTSQGSSAGSTVAS 1504	2347 RISSPSTASTKSSGSGKASYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKGLN 	2403OMNNGNGANKKVELSRMSSTKSSGGESDBSERPVLVRQSTFI	QY 2445 KEAPSPILRRKLEBSASFESLSPSSRPASPTRSQAQIPVLSPSLP 2489 DD 1624 ASASSQTGSTVTWGSSSTSGVSTSSASSTQPQMSTSQGSSAGSTVASSTTGLVSTSTV 1681	Oy 2490 DMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKR 2549 1682 PSSTGTMGSTSSGTVGSTISESSTAASASSQTGSTVTMGSSSTSGV 1727	QY 2550 EHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVS 2607 Db 1728 STSSASSGQPQMSTSQGSSAGSTVVSSTASPAASSTAPSSTGTMSSTSSGTVGSTMSQSS 1787	QY 2608 AKGIWRKIKENEPSPINSTSQTVSSGATNGAESKTLI 2644 Db 1788 TAASTTSHTGSTVTLGSSSTSSNQMSTSQGSSVGSTVASSTAGLVSTSTV 1837	QY 2645 YQWAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQ 2704 :	NVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSET-NESPIVE 2 :	ADST	Qy 2816 RDSKTDSTESSCTQSPKRHSGSYLVTS 2842 : : : : :	RESULT 8 T23327 adenomatous polyposis coli protein 1 - Caenorhabditis elegans	N'Alternate names: apr-1 profein C'Species: Caenorhabditis elegans C'Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999 C'Accession: T23327; T03822	R.Gardner, A. submitted to the EMBL Data Library, July 1996 A;Reference number: Z19727
alo (IMILATILY 20.4%; Fred. No. 28-13; 7; Conservative 247; Mismatches 811; Indels 454; Gaps TDIPSSQKQSFSFSKSSGQGSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRS :	360 TVVPGSSSTFASSTPIASSSSPGSTVTVAPGSSSTYGSSTPSASSSSGTMSTNSGSTGS 419 1241 GQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADS 1298 1241 GQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADS 1298 420TVTVAPVSSSTFGSSTPIASSSSSGSTVTVVSGSSSTYGSSTPSASSSS 468	ANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSSSARHKAVEFPS	1357 GAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSE 1408 :	PCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPXNKAPTAEKRE	1465SCPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSLSALS 1510 638 TITPEGSTASSPIGSTGSTGSTGSVATEVTSQSTVPSGSSLGTQSTNSSPSPSSLSPSTSGMS 697	1511LDEPFIQXDVELRIMPPVQENDNGNETESEQPXESNENQEKEAE 1554	KIIDSEKDLIDDSDDDDIEILEEGIISAMPIKSSRKGKKPAQTASKLPPPVARKPSQL 1	PVYKLLPSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPP 16	NELAAGEGVRGAQSGEFEKEDTIPTEGRST-DEAQGGKTSSVTIPE 17	LDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKP 1 Colora	TSPVKPIPONTEYRTRVRKNADSKONLINAERVFSDNKDSKKONLKNNSKDFNDKLPNNED 1 	1833 RVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEA 1892 1008TSSSGSP1014	KVTSHTELTSNQOSANKTQAIAKQPINRQPKPILQXQSTFPQSSKDIPDRGAATDEKLQ 	1953 NFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQAS 2005 1063PSTVSGSASSGSTATMGSTEASSTSGGSSTSPNPSQSTSFSTS-GATSSPGSS 1114	2006 GYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEK 2062 1115 GTTLTSISPSPSQSSTIGSSQGSTSPVVSTTSGDMTSQGSTQIPGSTGSTVTQPSTGS 1172.	2063 HSPRNMGGLLGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSS 2114

SPTMCAQVFNLPKSTESEHHQLTSQQQNTTHYSSGSANTMTRSDGATTVPMDNIITP -YSLKYSDBQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQS -TYLLNPILVHEQTPH	QY 1228 QNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVBDTPICFS	RESULT 9 T23330 hypothetical protein K04G2.8b - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999 C;Accession: T23330 R;Gardiner, A. submitted to the EMBL Data Library, July 1996 A;Reference number: Z19727 A;Accession: T23330 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Status: preliminary; translated from GB/EMBL/DDBJ A;Residues: 1-1188 <wil>A;Cross-references: EMBL:Z75712; PIDN:CAB00048.1; GSPDB:GN00019; CESP:K04G2.8b A;Experimental source: clone K04G2 C;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Genetics: A;Amp position: 1 A;Introns: 61/3; 113/2; 355/3; 551/3; 1069/3; 1163/3</wil>	Query Match 3.5%; Score 514.5; DB 2; Length 1188; Best Local Similarity 21.9%; Pred. No. 1.1e-13; Matches 289; Conservative 216; Mismatches 564; Indels 249; Gaps 52; QY 271 MATSGNGGSTTRMDHETASVLSSSTHSAPRRITSHLGTKVEMVYSLLSMLGTHDKDDM 330 1
A; Molecule type: DNA A; Residues: 1-1186 < WIL> A; Residues: 1-1186 < WIL> A; Residues: 1-1186 < WIL> A; Cross-references: EMBL: 275712; PIDN: CAB00045.1; GSPDB: GN00019; CESP: KO4G2.8a A; Cross-references: EMBL: 275712; DIDN: CAB00045.1; GSPDB: GN00019; CESP: KO4G2.8a A; Rechelment, C.E.; Downs, W.D.; Lin, R.; Wittmann, C.; Bei, Y.; Cha, Y.H.; Ali, M.; Prie Call 90, 707-716; 1997 A; Title: Wnt signaling and an APC related gene specify endoderm in early C. elegans embra; Reference number: 215051; MUID: 97433081; PMID: 9288750 A; A; Reference number: 215051; MUID: 97433081; PMID: 9288750 A; A; Rolecule type: mRNA A; Residues: 1-1186 < RCC> A; Cross-references: EMBL: AF013950; NID: 92338717; PIDN: AAC47747.1; PID: 92338718 A; Resperimental source: strain Bristol C; Genetics: A; Gene: apr-1; CESP: KO4G2.8a A; Map position: 1 A; Introns: 61/3; 113/2; 355/3; 551/3; 1067/3; 1161/3	Query Match Best Local Similarity 21.9%; Pred. No. 9.1e-14; Matches 289; Conservative 216; Mismatches 562; Indels 251; Gaps 52; QY 271 MATSGNGGGSTTRMDHETASVLSSSSTHSAPRALTSHLGTKVEMVYSLLSMLGTHDXDDM 330 Db 185SSSDENETTIHRTGSNTGGGGIYSQPRAGSSKRTSNVRHDVSDVDDE 50 QY 331 SRTLLAMSSSQDSCISMRQSGCLPLIOLLHGNDKDSVLLGNSRGSKBRARASAALHN- 389 Db 51 EEHYARPREDTAIFV-DDAITVLLSGIHFEHKRDIVPTBEDDNKLRELHEK 100 QY 390IIHSQPDDKRGRREIRVLHLLEQIRAYCETCWBWQEAHERGMDQDKNPWPAPVEHQI 446 Db 101 IPALITSESDVNKRRRIKKALPASNCW	OY 505 LTNLTFGDVANKATLCSWKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLR 564 Db 210 LTNLTYGQIHSKRLCSYDGFIRCVV-RIVIESPNITQVYAGLIRNLSWNADSGMSEALQ 268 CY 565 EVGSVKALMECALEVKKES-TLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYR 623 1	QY 802 DTWRHDDMRSDNFNTGNWTVLSPYLNTTVLPSSSSSRGSLDSSRSEK-DRSLERERG 857 Db 500 QTPQVDQRSSSLPRHFAVQRNGFYMAQSYNQOMDQHQQQQMIYQLQQQQ 549 QY 858 IGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCV 915

qq	101 IFALTISESDVNRKERLKKALPASNCVRBOVYYLRRKPSTPPASYYHRL 149	Db	
λō	CPAVCVLMKLSFDEEHRHAMNELGG	8 7	o r
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à i	LINLTFGDVANKATLCSMKGCMRALVAQLKSESBDLQQVIASVLRNLSWRADVNSKKTLR	RESULT 10 A43359	(0.000
an .	DINITYGQIHSKKKLCSTDGFIKCVV-KIVIBSFNIIQVIAGELKNLSMNADSGMSBALQ 20	C,Species	Rattus
ý t	565 BVGSYKALMBCALEVKKES-TLKSVLSALMNISAHCTENKALICAVDGALAFLVGILIYK 623 269 D. THURIT GRANNERHYPPHYMATIKALMNITH HIN HIN HIN HIN HIN HIN HIN HIN HIN HI	C,Dace: 31-Dec-19 C,Accession: A433 R;Langkopf, A.; H	ion: A433 of, A.; H
3 8	SOTITIALIESGEGILRINGSELIATHEDHROLLERENNCLOTLLOHLKSHSLTTVSNACGT 68	J. Biol. A; Title:	Chem. 26 Microtub
전 전	ARFTSLVDSATGLIKYVSQYLANTSTHLELRSLLITRMLTLKSASFTCVINTLGA	A; Referer A; Accessi	ion: A433
ŏ	684 IWNLSARNPKDQEAL-WDMGAVSWIKNLIHSKHKMIAMGSAAALRNIMANRPAKYKDANI 742	A,Molecule type: A,Residues: 1-277 A:Cross-reference	le type: ss: 1-277 reference
qq	383 IANLIVKDPHMQQMIRQDMAAVQQLNVLRNSNRDDIRTAVKSVLNTLNQPCSHRYGDM 440	A;Note: seq R:Cravchik,	sequence
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qa		A, Accessic	
š Š	DINRHDDNRSDNFNTGNMT	A;Molecule type: A;Residues: 73-3	ie type: es: 73-36 popposp',
qq	3	A; Cross-:	A; Cross-reference
\$ £	858 IGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCV 915	A; Experit C; Superf C; Keyword	A,Experimental so C,Superfamily: mi C,Keywords: micro
3 8	THE STATE OF CANDITION THE STATE OF THE STAT	Ouerv	Match
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ò	976 RGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPIN 1026	ò	0dv 609
QQ	656 SPTMCAQVFNLPKSTESEHHQLTSQQQNTTHYSSGSANTWTRSDGATTVEMDNIITP 712	qq	1 MDG
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٥٨	1073 TTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGI 1121	ò	701 MG2
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٥٨	1175OPIDYS-LKYATDIPSSQKQSFSFSKSSGGSSKTEHMSSSSBNTSTPSSNAKR 1227	λΌ	802 DI
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Š	1228 QNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFS 1272	δ	839
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οχ	1273RCSSLSSLSSAEDEIGCNOTTOEADSANTLOIAEIKGKIGTRSAEDP 1319	ò	877 GE(
QQ	989 TQFDDGVDAQLTIDCSMISSGSGSSQRNETTTSRDSKALATSTPKGS 1036	Dp	322 SL
ογ	1320 VSEVPAVSQHPRIKSSRLQGSSLSSBSARHKAVEPPSGAKSPSK-SGAQIPKSPP 1373	λο -	932 SN
Db	1037 ASSLPGVRQATRVSTNGKSRLPVPKTNGSLVDKNPKPIIASRRPRLPPKP 1086	qa	382 GE
δλ	1374EHYVOETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPS 1421	ò	974

	DP QC	1087 TLLKDKHYPEEDSIENÇTRDDIIYVNAPVVEAEQERIYMNALKQQK 1132
	දු දු	1422 DLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPROXXAPTAEKRESGPKQAAV 1472 ::
	RESULT 10 A43359 C. A43359 C. Species 31. C. Accession C. A. Tingkopf, J. Biol. Off, J. A. Title: Mi A. Molecule A. Molecule A. Residues: A. Cross-ref A. Note: see A. Note: see A. Note: see A. Molecule A. Molecule A. Residues:	RESULT 10 A43359 microtubule-associated protein MAPIA - rat microtubule-associated protein MAPIA - rat C.Species: Rattus norvegicus (Norway rat) C.Species: Rattus norvegicus (Norway rat) C.Species: 11-Dec-1993 #sequence revision 31-Dec-1993 #text_change 13-Aug-1999 C.Accession: A43359, S22108 A.F. Hammarback, J. 16561-16566, 1992 A.F. Hannarback, J. 16561-16566, 1992 A.F. Hannarback, J. 16561-16566, 1992 A.F. Reference number: A43359, MUD:92355629, PMID:1379599 A.F. Reference number: A43359, MUD:92355629, PMID:1379599 A.F. Residues: 1-274 < LAN> A.F. Residues: 1-274 < LAN> A.F. Residues: 1-274 < LAN> A.F. Residues: 1-274 < LAN> A.F. Reference extracted from NCBI backbone (NCBIN:111039, NCBIP:111040) B.Coss-references: GB:MB3196, NID: g205537, June 1992 A.F. Reference number: S22108 A.F. Reference number: S22108
,	A)Residus A)Residus A)Residus 'WLKRNMCI A)Cross-1 A)Experin C;Superfe C;Keyword	A, Status: preliminary A, Status: preliminary A, Molecule type: mRNA A, Residues: 73-364, 'NRLS', 370, 'QKN', 374, 'PSPKGL', 381-751, 'RSMMSQMNAQRR', 764, 'D', 766, 'LRN A, Residues: 73-364, 'NRLS', 370, 'QKN', 374, 'PSPKGL', 381-751, 'RSMMSQMNAQRR', 764, 'D', 766, 'LRN A, RANDOPPROSP', 851, 'V', 833, 'NST', 855, 'LPHRWLRIN', 865, 'W', 867, 'HSQLPDGGD', 877, 'Q', 879, 'I A, EXPARIMENTAL SOUTCE: STRAIN SPIRAGE Dawley A, EXPARIMENTAL SOUTCE: STRAIN SPIRAGE DAWLEY C, Superfamily: microtubule-associated protein C; Keywords: microtubule binding; phosphoprotein
	Query M Best Lo Matches	7 Match Local Similarity 18.7%; Pred. No. 1.2e-11; nes 542; Conservative 359; Mismatches 1039; Indels 958; Gaps 133;
	çç Q	609 VDGALAFLVGTLITYRSQTNTLAIIESGGGILRNVSSLIATN 649
	Sy Sy	650EDHRQILRENNCLGTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWD 700
	S S	701 MGAVSMLKNLIHSKHKMIANGSAAALRNLMANRFAKYKDANIMSPGSSLPSLHV 754
	Qy	755RKQKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVF 801 142 KIRLPDASRKAKRSIEEACLTLQHLNRLGIQAEPLYRVVSNTIEPLTLFHKWGVGRLDMY 201
	QX	802 DINRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSR 838 202 VLNPVKDSKEMQPLMQKWAGNSKAKTGIVLANGKEAEISVPYLTSITALVVWLPANPTEK 261
	දු ස	839GSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKR 876 262 IVRVLFPGNAPQNKILEGLEKCRHLDFLRYPVATQKDLAAGAVPANLKPSKIKHRADSKE 321
	ار م	877 GLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTH 931 :
t.	ે ઇ	932: SNIYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGY 973
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ą	1473 R	
<u></u>	1890 S	SEAKVTSHTELTSNQQSANKTQALAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAA 1946
ð	1522 G	GETLDQEARTAEQKDETLKEDKTQGQKSSFVEDKTTTSKETVLDQKSAEKA 1572
<u>≽</u> ,	1947 -	H
ō	1573 D	SVEQQDGAALEKTRALGLEESPAEGSKAREQEKKYWKEQDVVQGWRETSP
<u>⊁</u>	2000 -	SKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECI-SSAMPKK 2050
ą	1631 G	GQKEPVPAWEGKSPEQEVRYWRDRDITLQQDAYWRELSCDRKVWFPHELDGQGARPRYCE 1690
≯	2051 K	MGGILGE
Q.	1691 E	ERESTFLDEGPDEQEITPLOHTPRSPWTSDFKDFQEPLPQKGLEVERWL 1739
≽	2103 A	AIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKP 2158
Q	1740 Å	BSPVGLPPEEDKLTRSP 1758
>-	2159 F	TSNKGPRILKPG
۵	1759 F	EIISPPASPPEMTGGRVPSAPGGESPVPDTESTAPMRNEPTTPSWLAEIPPWVPXDR 1816
λ.	2187 -	GIKGGKKVYKSLITGKVRSNSBISGOMKQPLQANMP 2222
Д	1817 P	PLPPAPLSPAPAPAPPTPAPEPHTPVPFSWGLAEYDSVVAAVQEGAAELEGGPYSPLGKDYR 1876
>	2223 S	SISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSE 2263
Д	1877 K	AEGEREGEGGAGAPDSSSFSPKVPEAGESLATRDTEQTEPEQREPTPYPDERSFQYADI 1936
>-	2264 -	- 1
Ω	1937 YI	EQMMLTGLGPACPTREPPLGASGDMPPHLSTKEBAAGCNTSAEKETSSPASPQNLGSDT 1996
>-	2309 P	SRPAQPLSRPIQSPGRNSISPG
Ω	1997 Pi	PAFSYASLAGPÄVPPRQEPDPGPNVEPSITPPAVPPRAPISLSKDLSPPLNGSTVSCS 2054
>-	2349 SS	PSTASTKSSGSGKMSYTSPGRQMSQ
۵.	2055 PI	PDRRIPSPKETGRGHWDDGTNDSDLEKGAREQPEKETRSPSPHHPMPMG 2103
>-	2406 NC	NGNGANKKVELSRMSSTKSSGS 2427
۵	2104 HS	: SSLWPETBAYSSLSSDSHLGSVRPSLDFPASAFGFSSLQPAPPQLPSPABPRSAPCGSL 2163
5.	2428	-ESDRSERPVLVROSTFIKEAPSPTLRRKLEESAAFESLSPSSRPASP- 2474
0	2164 A	FSGDRALALVPGTPTRTRHDEYLEVTKAPSLDSSLPQLPSPSSPGGPLLSNLPRPASPA 2223
.	2475	TRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEY 2517
0	2224 LS	: : ERFPPGLEAAEQSAEGLGSGKESAAHS
_	2518 NI	NDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRR 2566
0	2279	PSASLDLAPAPAPAPAPAPAPAGLPGDLGDGTLPCRPECTGEL 2318
_	2567 TC	TGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEF 2620
0	2319 TE	TKKPSPFLSPSGDHEANGPGETSLNPPGFVTATAEKEEAEAPHAWERGSWPEGAERSS 2376
		265
•	2377 RE	RPDTLLSSEQPLRPGKSSGGPPCSLSSEVEAGPQGCATDPRPHCGELSPSFLNPPLPPST 2436

	1522 YSGYDCKFTYPAPTRESEABESTSRIPTIPEABECGGGEAGYPEEPDSGESSTRAPDO 1221 1522 VSTSSRIAGRACHOTAKLAP
4 6 6 6 6 6 6	B & B & B & B & B & B & B & B & B & B &
Qy 2655 EDVWYRIEDCPINNPRSGR-SPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNG 2709 2437 DDSDLSTEEARLAGKGGRRRVGRPGTCPMADETPPTSASDSGSSGSDVPPE 2493 Qy 2710 SVPMRTVGLENRLTSFIQVD-APDQKGT-EIKPGQN-NPVPVSETNESPIV 2757 Db 2494 TEBCPSITAEAALDSDEDGFLPVDXAGGVSGTHHPRPCHDPPPTPLDDPRPSPRPPDVC 2553 Qy 2758 ERTPFSSSSSSKHSSPSGTVARRVTPN	PESCILT 11 174513 17451

2189 KGGKKVYKSLITGKVRENSELSGGMKQPLOANMPSISRGRTMIHIPGURASSSSTSPVSK 2079	GRIMIHIPGVRNSSSSTSPVSK 2248 A;Gene: SP1772	2099	2301 Matches 418;	STSPTEVHTSSETKPSLSASST 2151 QY 514 ANKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVK 570		2205 QY 571 ALMBCALEVKKESTLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTY	2396 Db 129 AAATEATAKKVEEDRKKPASDYVASVTNVNLOSYAKRRKSVDSIEQLLASIKNAAVP	2265 Qy 623	2443 Db 187	TPINILSESSTVETPKTSSEVSL 2325 QY 671 SHSLTIVSNACCTLWNLSARNPKDQEALMDMGAVSMLKNLIHSKHKMI 718	LPDMSLS 2494 Db 241 TYTVTYVNPKTNDLGNISSMRPGYSIYNSGTSTQTMLTLGSDLGKPSGVKNYITDKNGRQ	: LVTSSV- 2384	2545 Db 301 VLSYNTSTMTTQGSGYTWGNGAQMNGFPAKKGYGLTSSWTVPITGTTFTPYAARTD	2430 Qy 741NIMSPGSSLPSLHVRKOKALEAELDAOHLSETFDNIDNLSPKASHRSKORHKOSLY	2601 Db 361 RIGINYFNGGGKVVESSTTSQSLSQSKSLSVSASOSASASASTSA-	2484 OY 797 GDYVFDINRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERER	PT 2623 Db 406	2544 Qy 857 GIGLGNYHPATENPCISSKRGLOISTTAAOIAKVWEEVAAIHTSORDRSSGSTTTEIHCVT	2679 Db 453ASESASTSASASASTSASASTSASASTSASASTSASASTSASASASTSASTSA	2604 QY 917 DERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGY	2733 Db 502 SESASTSASASASASASASASASGSASTSTSASASASTSASASASTSASASISASASSSA	2662 QY 974 GKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSD	2793 Db 562 STSASESASTSTSASESASTSASASASTSASASASTSASASASTTSASASTSASASTTSASASTSA	2709 OV 1034 BOLNSGROEDSONERWARPEXHTTERETXOGROEDSCHOOLING TOTAL TO	2843	3	בייני בייני בייני כי בייני ביי
	KGGKKVYKSLITGKVRSNSEISGOMKOPLOANMPSISRGRIMIHIPGVRNSS	2079	ZZZZZ NGFFENNIFASNAFSEGQIAIISFRGARFSVKSELSFVARQISQIGG:	2100STPSTTSQSVTSTVPBTSKSTVLSSEAPVTSTSPTEVHTSSETKP	2302 SGSRDSTPSRPAQOPLSRPIOSPGRNSISPGRNGISPPNKLSQL-PRTSSPST-	2152 TGDTNSTTPSTSSLASVKSTSAPEGTSASVAPVKLSSLSPDVSQPSTKTFDATE		2206 SSTVQASETSSGTSVKSTSEPESHVTKLSITSSNPSSSVPVTSPKSTEQPTST	2397 ASKGLNQMINGNGANKKVELSRMSSTKGSGSESDRSERPVLVRQSTF	2266 TPSGQSLTPMNSNSEVLTTSEPHVLSSSLSPDVSQSSTTPNNLSESSTVETPKTSSEVSL	IKBAPSPILRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPS	NSEEPSTTEAPTILSPDILSTTTNNLSQSSTVSTEDRSEISSENSEKPISAPE	2495 THSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSG	2385 THVASSSPDVPTESSEPDDLTGSSTENIPEASSKQIISSTPIPDTI	2546 TWKREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAK-SEDEKHVNSISGTKQS	2431 TASEEPTKSTSMSPDLSTTSNVLSESSTTPESSSKSPVSSTEGISVVTSTEFS	K	2485 KVPESTISSVLEEDLTKTTPSPILËETTTASETSEPLTEDSLTVSVRIHELTISSENVPK	2624 NSTSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNP-RSGRSFTGNT	2545 ESESTITSSESSKPSQEPAGILISTVVVPISSVSLITASBIEALTSNIPFKQGRIPITIS	2680 PPVIDSVSEKANPN-IKDSKDNOAKONVGNGSVPMRTVGLENRLTSFIQV	2605 PKSLVKSTTSPSTVTSSEPSESTKRTTVSTTVSTTTPTEETTTSESLILTAAPSKPTE	2734 KGŢĒIKPGQNNPVPVSEŢNESPIVERTPFSSSSSKHSSPSGTVAARVTPFNYNPSPRKS	STTESSEAPTTPAKTSETKPSNVSSTSRKSTENVETSTSQSGSL		: : : : : : : : : : : : : : : : : : :	

1329 HPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKS-GAQTPKSPPEHYVQETPLMFSRC 1387 1388 TSVSSLDSFESRSIASSVOSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPQTAQ 1447 1213 ----SSSENTSTPSSNAKRQNOLHPSSAQSRSGQPQKAATCKVSSINOFTIQTYCVEDTP 1269 ICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQ 881 TSASESASTSASASASASASASTSASASTSASASTSASASTSASASTSAS 774 SASISASESASTSAS-----ASASTSASASASTSASASASTSASASAS 1154 EEBERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMS-740 Ωp ò g ò g à d ઠે Call wall surface anchor family protein [imported] - Streptococcus pneumoniae (strain TI c.Species: Streptococcus pneumoniae ().Species: O3-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C; Accession: E95206 F. Fettellin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heid nson, T.; Hickey, E.K.; Holt. O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, on J.D.; Pickey, E.K.; Holt. I.E. Science 293, 498-506, 2001 F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A; Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae. A; Accession: E95206 A; Status: preliminary A; Molecule type: DNA A; Redidues: 1-4776 < KUR> A; Cross-references: CB: AE005672; PIDN: AAK75846.1; PID: 914973269; GSPDB: GN00164; TIGR: SP4 A; Experimental source: strain TIGR4

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941 ASTSASESASTSASASTSASASTSASASTSASESASTSASASTSSASASAS 998	1448 TKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLS 1507 	1508 ALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSEKDLLDDS 1567	1568 DDDDIBILBECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQ 1627 	KHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKR	SASASTSASESASTSASASASTSASASASTSASASASTSASASASA	1688 DIIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIM 1747	1748 DQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSD 1807	1808 NKDSKKONLKONSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDF 1867 :	DDDDVDLSREKABLRKAKENKESEAKVTSHTELTSNQOSANKTQALAKQPINRGQPKPIL	1939 ASISASASASASASASISABASASISASASISASASISASASISASA 1401 1928 QKQSTFPQQSSKDIPDRGAATDEKLQNPAIENTPVCFSHNSSLSSLSDIDQENNNKENEPI 1987		1988 KETEPPDSQGEPS-KPQASGYAPKSFHVB-DTPVCFSRNSSLS-SLSIDSEDDLLQECIS 2044 1988 KETEPPDSQGEPS-KPQASGYAPKSFHVB-DTPVCFSRNSSLS-SLSIDSEDDLLQECIS 2044 1988 KETEPPDSQGEPS-KPQASGYAPKSFHVB-DTPVCFSRNSSLS-SLSIDSEDDLLQECIS 2044	2045 SAMPKKKRPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAI 2104	2105 QEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFTSNKG 2164	2165 PRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQANM 2221 	PSISRGRTMIHIPGVRNSSST8PVSKKGPPLKTPASKSPSEGOTATTSPRGAKPSVKSE	LSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPNK	SASASIZARSABABISABASIZASABISASABSABISABESASIZISABARIS INI LEQUEPRISSESTASIKSGGGGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKGL 240 : :: ::: :::		2402 NOMNIGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESAS 2461,	2462 FESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEVNDGR 2521	
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A;Map position: 2 A;Introns: 36/2; 92/2; 182/2; 272/3; 344/2; 426/2; 490/1; 541/2; 700/3; 770/3; 1286/3; 15 hypothetical protein F07All.6b - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 29-Oct-1999
C;Accession: T20532; T27777
R;Palmer, S.
submitted to the EMBL Data Library, October 1995
A;Accession: T20532
A;Reference number: Z19287
A;Accession: T20532
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A;Accession: T2072 < WIL>
A;Residues: Preliminary; translated from GB/EMBL/DBJ
A;Residues: 1-2722 < WIL>
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A;Residues: Data Library, March 1996
A;Reference number: Z20417
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OECUS PYRSRGANGSETNRVGSNHGINONVSQSLVSSFVNRIDEIVELNQKARASYER PTNYSERYSEEDGHEEBER PTNYSIKYNBEKRHVDG
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<i>ኢ</i>	1917	FPOSSKDIPDRGAATDEKLONFAIEN 195
Ω	1444	PLSPPVTAKSSVSSIDDPSIRDEFSMNSAADSPMSTTGRPMVLTKAAMKAFNS 1496
≿ :	1959	TPVCFSHNSSLSSLSDLDOBNNNKENBPIKETEPDDSOGEP 1999
ą	1497	TPPKKKNSSSGQHDSSSGSSSBSSSSBGSTSSDBSSDDEVPKQTEFVTSIPVVASDNGSP 1556
λί	2000	SFHVEDTPVCFSRNSSLSSLS
ð	1557	ENVVVETPSIVSQTPREPEPFTISEQSSESEPEAVPECPEASVEPQMETS 1606
≵:	2054	SRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVS 2113
ą	1607	ONVEPVSEHEDSHEHGDSEVAVESQQQP-LEHQEEKEELENKILD 1651
≵ı	2114	S
ð	1652	VAAEHHEEGVQGDEDSVESSIPAPSDBPDPVTQAQEKSAHTLISDQETDQAV 1703
≱:	2161	
Ð	1704	QSIFDEBEADEPPQYPDFGISTNEKEVSGKDPHNIKPTEPLNNGHTDLLFSPSSSAHASE 1763
≱:	2173	-KSTLETKKIESESKGIKGGKKV-YKSLITGKVRSNSEISGQMKQ 2215
Q	1764	KOSTKSEDDMEEDSELVVMEKEVPMEQVIAQEVHVPSEPSPMEEEVKLETSPVPKEEPIK 1823
≱	2216	KGPP
۾	1824	MEESPEGTPTPDLISNNESQDTPGAVNNHLHENHDAVGTPIQLQPASGHQVAQPS 1878
≥ -	2271	PRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSIS 2330
۾	1879	PRPAVAPDSQQNGPVLVSQQSQPSPMSSQQSDMAQNLIL 1917
<u>~</u>	2331	PGRNGISPPNKLSQLPRISSPSTASTKSSGGKMSYTSPGRQMSQQNLTKQTGLSKNASS 2390
ą	1918	SSKDINDLAAKLHKNPBALAQATRGDCSGIFQHLLLHAQGNGQNMTPEMLQLKAAFF 1974
>	2391	IPRSESASKGLNOMN NGNGANKKVELSRMSSTKSSGSESDRSER 2434
Ą	1975	AQQQENEANQMMQAKKKQQTINKDRIKEQERVKRMYEENERKVEEDRREKQRKEEERQRL 2034
≻	2435	PTL-
Ą	2035	
≽	2467	SVQAGGWRKLP 2508
Ą	2095	ATNGVLHLPTQSIQRPSS-TASTSSNPFKAPLQPSASVNQNTIDPAEIEEIRVQRWFYKP 2153
>-	2509	PNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTW 2564
Д	2154	LICMSABEAATVMAVASSDPNPPATSTVDLAAMLQQLQAAQAAQAAQQVPVVTTA 2207
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Д	2208	STPNPLSNLETLISTASLANLATGGALNPLSMLALTSSLNQSSPVYQGIARVLLIMMGQ 2267
>	2623	TNSTSQIVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGN 2678
ڼ	2268	MIATHQTSELLATMN-QQETLMALLAARNGLPFAMPQONQQPQMPAQGG 2315
γ	2679	TPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGT 2736
Д	2316	FAIPTVLPHMSLKRNAKDQLSVGGVSDRKKSCPLHAMIGQGQQPPPPQQPMQ 2367
>-	2737	275
Д	2368	AVAPAPPRSPSPPRKSMFENLPPEMKËKNËMPRKEILRRLDIILLEELGAEDEEDQKPDL 2427

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OY 2758 ERTPFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNT 2813		
2428 KQIPTSEBDTDDSKADSMGAEGSAFRRILSRSSTWGNNSGSPSASGT 2474	1360	PLMFSR
2814 KKRDSKIDSTESGGIQSP 2831	Db 806 IPPTHD	IPPTHDEMMAPRGTPPSRRSSETWVPLRSPPFGTPIQNLLTMPIVPPPHLIAAT 859
2475TSPSTSSSTSSGPDSP 2490	1387	CTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLFDSPGQTMPPSRSKTPPPPPQTA 1446
	Db 860	SIGTHSVSSAHSTP-RHSISGTPVH-CEPSNSKTSQPPTP 898
RESULT 14 B89320 protein F07All.6 [imported] - Caenorhabditis elegans	Qy 1447 QTKREV ::: Db 899 KSRPEK	QTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSL 1506 :::
cies: Caenorhabdilis elegans e: 10-May-2001 #sequence_revision 10-May-2001 #text_change 10-May-2001 pssion: Pss230	1507	
The C. elegans Sequencing Consortium. The C. elegans Sequencing Consortium. 2012-2018, 1998	Db 954 VAQIMS	
le: Genome sequence of the nematode C. elegans: a platform for investigating biolog brence number: A75000, MUID:99069613, PMID:9851916 3: see websites genome wustl.edu/gsc/C elegans, and www.sanger.ac.uk/Projects/C ele	Qy 1538 -ESEQP : Db 1011 KEKERK	-ESEQPKESNENQEKEAE 1554
999; SCience 283, 2103, 1999;	Qy 1555	KTIDSEKDLDDSDDDIELLEECIISAMPTKSSRKGKKPA 1595
A.Residues: 1-2738 <sto> A.Cross-references: GB:chr_II; PIDN:CAA93781.1; PID:g3881547; GSPDB:GN00020; CESP:F07A11 A.Genetics:</sto>	1596	
Length 2738;	Qy 1656 SLSDLT t Db 1165 QQRRVL	SLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGG 1703
CONSELVATIVE 325, Mismatches 891; Indels 817; Gaps SDNFNTGNMTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENP	Oy 1704 KTSSVT : : Db 1224 EKGELT	KTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKN 1763 : :
GISSKRGLOISTIAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSA	Qy 1764 QLDGKK Db 1284 SEDAAA	QLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNMLNABRVFSDNKDSK 1812
B AHTHSNITVRFTKSENSNRTCSMPAKLEYKRSSNDSLNSVSSNDGYGKRGOMKPSIESYS SHIP STATEMENT STATEMENT SMPTAKLEYKRSSNDSLNSVSSNDGYGKRGOMKPSIESYS SHIP SMPTANGY SM	Qy 1813 KQNLKN : :: Db 1344 RSRRQS'	KQNLKNNSKDFNDKLPNNEDRVRGSFAFOSPHHYTPIEGTPYCF 1856 : :
EDDESKTCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQINSGRQS	Oy 1857 SRNDSL. :: : Db 1402 TKRSSL	SRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQOSANKTQAIAKQ 1916 :: : : : : : :: : :: : TKRSSISDHENLISPRQRNRTTSSTS-TATTSSKHEALSIPEK 1443
	Qy 1917 PINRGQ Db 1444 PLS	PINRGOPKPILOKOSTFPQSSKDIPDRGAATDEKLONFAIEN 1958 ::
QECUSPYRSRGANGSETURVGSNHGINQNUSQSLCQEDDYEDDK	Qy 1959 TPV Db 1497 TPPKKV	TPVQFSHNSSLSSLSDIDQENNNKENEPIKET 1990
PINYSERYSEBEQHEBEERPTNYSIKYNBEKRHVDQPIDYSLKYATDIPSSQKQSFSFSK	Oy 1991 EPPDS 1 Db 1557 EPVTSII	EPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDL 2038
1200 SSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSQQPQKAATCKVSS 1253	Qy 2039 LQEC-IS : Db 1607 VPECPEA	LQEC-ISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSE 2097
INQETIQTYCVEDT : : :	Qy 2098 NFDWKAIQ Db 1660 BLENKILD	NFDWKAIQBGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSFFHLTPDQE 2155
ABIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEPPSGAK PSTSGGITTPRSSQPPPLMSPVSRHNSMSSTGRPASIQTLRHQSVMPPPDVSIPPPP	Qy 2156 EKPFT- : Db 1704 KSAHTL:	EKPFT 2172 :

ILOKOSTFPOSSK---DIPDRGAATDEKLONFALEN 1958 ENEP-IKETEPPDSQGEPSKPQASGYAPKSFHVED- 2016 IDSEDDLLQECISSAMPKKKKPSRLKGDNEKHSPRN 2067 DSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQ 1429 ------AQTKREVPKNKAPTAEKRESGPK 1468 ADTLLHFAT---ESTPDGFSCSSSLS----ALSLD 1512 ILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKP 1609 PGDDMPRVYCVEGTPINFSTATS--LSDLTIESPPN 1667 IPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILA 1725 VQQASASSAPNKNO--LDGKKKKPTSPVKPIPQNT 1783 SDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFD 1841 -TPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSI 1254 SLSSAEDEIGCNOTTOEADSANTLOIAEIKGKIGTR 1314 GSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPE 1374 | :|| :| :| VLDAVPRIPSRERS----SSASSPEMKDGLPRIPSR 469 DFDDDDVDLSREKAELRKAKENKESEAKVTSHTELT 1901 EVD-----SKSRLSPRRSRSGSSPBVKDKPRAA 643 SPEPKTKSRTPPRRESSRSSPELTRKARLSRRSRSA 742 FSPEHKELSNSPLRENSFGSPLEPRNSGPLGTERNT 377 -RPRSRSPSSPELNNKCLTPQRERSGSE-SSVDQKT 559 SPSLQSKS-----QTSPKGGRSRSSPVT 138 MSPEQSRFQSDSSSYPTVDS-NSLLGQSRLETAESK 197 FPVQDRPESSLVFKDTLRTPPRERSGAGSSPETKEQ 257 SPQERSE-----SDSSPDSKAKTR---e 419.5; DB 2; Length 1791; | No. 1.5e-09; |ismatches 742; Indels 537; Gaps

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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

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OM protein - protein search, using sw model

Run on:

August 25, 2004, 16:58:21; Search time 32.5 Seconds (without alignments) 4554.937 Million cell updates/sec

US-09-442-489F-2
14575
1 MAAASYDQLLKQVEALKMEN.......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

÷	Description	P25054 homo sapien	78 rattu	Q61315 mus musculu		drosc		mus n	mus n	P78559 homo sapien	rattı	homod	homo		rattı	Q12955 homo sapien	Q8nez4 homo sapien	gall	Q9qyx7 mus musculu	homo		homo	mus n	mus m	homo	pan t	homo	mus mu	Q9pu36 gallus gall	h pe	ጟ	caen	pongo 8	Q02224 homo sapien
SUMMAKIES	ID	APC HUMAN	APC RAT	APC_MOUSE	MAPA RAT	SPEN_DROME	MINTHUMAN	MINT MOUSE	ZEP1 MOUSE	MAPA_HUMAN	PCLO RAT	ANK2 HUMAN	PCLO HUMAN	CENF_HUMAN	MAPB RAT	ANK3 HUMAN	MLL3 HUMAN	PGCV CHICK	PCLO_MOUSE	KI 67 HUMAN	HRX_HUMAN	MAPB HUMAN	MAPB_MOUSE	NCR1_MOUSE	NCR1_HUMAN	ATRX PANTR	TCOF HUMAN			PPRB HUMAN	GOB1 HUMAN	UN89 CAEEL	ATRX_PONPY	CENE_HUMAN
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PGCV MOUSE	ATRX HUMAN	BPA1 MOUSE	AMYH_YEAST	NKCR MOUSE	NKCR HUMAN	P531 HUMAN	NCR2_MOUSE	YJH6 YEAST	ANC1 CAEEL	BRC2_RAT	SC16_YEAST
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356	355	352	350.5	350	350	350	349	345.5	345.5	345	344.5
34	35	36	37	38	39	40	41	42	43	44	4 Ծ

ALIGNMENTS

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             MEDLINE=93244793; PubMed=1338691;
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Nakamura Y., Horii A.;
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mutations in very well differentiated adenocarcinoma and signet-ring
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                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF 2-55.

MEDLINE=20384842; PubMed=10926498;
Day C.L., Alber T.

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"Mobile F. S., Spycher M., Heellana R., Ammann R., Ammann T., Roth J.,

"Mobile F. S., Spycher M., Heellana R., Ammann R., Ammann T., Roth J.,

"Mobile F. S., Spycher M., Heellana R., Ammann R., Ammann T., Roth J.,

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"Mobile F. S., Spycher M., Heellana R., Shy Heelland R.,

"Momile F. S., Spycher M., Mobile J., Spycher P., Marchie C., Susca F., Gentile M.,

"Momile F. S., Pilas S., Prete F., Marchi C., Guanti G.,

"Momile J., S., Prete F., Marchi C., Guanti G.,

"Momile F., Molie B., Mobile J., Waine M., Wasen H.F.A., Tope C.M.J.,

"Mobile F. J., Mobile J., Mobile J., Waine J., Wasen H.F.A., Tope C.M.J.,

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"Morial M., Mishlo J., Mobile J., Mobile J., Wasen J., Walle M., Walle J., Mobile J., Mobile J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J., Walle J.,
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                                                         24. BAERSSQNKHETGSHDAERQNEGQCVGEINMATSGNGQGSTTRMDHETASVLSSSSTHSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTELETEASNMKEVLKQLQGSIEDETM
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Wnt signaling pathway? Anti-oncogene; Phosphorylation; Coiled coil;
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62 COLLED COLL (POTENTIAL).
260 COLLED COLL (POTENTIAL).
493 ARM 1.
589 ARM 3.
636 ARM 3.
631 ARM 5.
723 ARM 6.
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                                  and Fischer 344/N;
                                                MEDLINE=95148647; PubMed=7846077;
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InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 4.
SWART; SM00185; ARM; 5.
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MUTAGENESIS.
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                                             SNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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STRAIN=Fischer 344/N; TISSUB=Brain;
MEDLINE=96116966; RubMed=8563176;
MEDLINE=9610966; RubMed=8563176;
TOYOTA M., UShijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A., Sugimura T., Nagao M.;
"CDNA cloning of the rat APC gene and assignment to chromosome 18.";
Mamm. Genome 6:746-748(1995).
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2003 (Rel. 42, Last annotation update)
Adenomatous polyposis coli protein (APC protein).
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77:70:90

Aug

NFDWKAIQEGANSIVSSLHQ-AAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEE ASKGINOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKL -NNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD KPFTSNKGPRILKPCEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGGMKQP LOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKP PSQNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGG PPPPQTAQTKKEVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPD GFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTID GFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETEPEQPEESNENQDKEVEKP-D NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQE SVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGI AQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSH

Thu Aug 26 06:02:22 2004

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                                                                                                                    Isoid=Q61315-4; Sequence=VSP 004116, VSP 004117,
-!- TISSUE SPECIFICITY: Expressed in liver, spleen, kidney, heart,
lung, brain, stomach, intestine, testis and ovary.
-!- PTM: Phosphorylated by GSK3B (By similarity).
-!- SIMILARITY: Contains 7 ARM repeats.
                           Event=Alternative splicing; Named isoforms=4;
                                                                                       IsoId=Q61315-3; Sequence=VSP_004117;
Name=4;
                                                                       IsoId=Q61315-2; Sequence=VSP_004116;
                                                 IsoId=061315-1; Sequence=Displayed;
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             ALTERNATIVE PRODUCTS
  (By similarity)
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             2457 EESASFEGLSPSSRPDSPTRSQAQTPVLSPSLPDMSLSTHPSVQAGGWRKLPPNLSPTIE 2516
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STAIN-CS7BL/6J, and CAST/EI; TISSUE-Brain;
MEDLINE-9226101; Pubmed=1350108;
Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
Luongo C., Gould K.A., Dove W.F.;
Multiple intesinal neoplasia caused by a mutation in the murine
homolog of the APC gene. ;
Science 256:668-670(1992).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
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Dicker F., Lambertz S., Reitmair A., Ballhausen W.G.;
"The murine APC gene: alternative splicing of 5' untranslated
                                                                                                                                                                                                                                                                                                                                                                   APC_MOUSE STANDARD; PRT; 2845 AA.
Q61315; Q62044;
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Adenomatous polyposis coli protein (APC protein) (mAPC).
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DR RMEL; U02937; AAA03443.1; -.

DR ROSS, 102248; 3BCT.

DR GO; GO:0005737; C:cytoplasm; IDA.

DR GO; GO:0005634; C:nucleus; IDA.

DR GO; GO:000952; P:anterior/posterior pattern formation; IMP.

DR GO; GO:000992; P:anterior/posterior pattern formation; IMP.

DR GO; GO:000992; P:anterior/posterior pattern formation; IMP.

DR GO; GO:000992; P:anterior/posterior pattern formation; IMP.

DR GO; GO:000992; P:anterior/posterior pattern formation; IMP.

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DR GO; GO:000992; P:anterior/posterior; IMP.

DR GO; GO:000992; P:anterior/posterior; IMP.

DR GO; GO:000992; P:anterior/posteri HIGHLY CHARGED.
Missing (in isoform 2 and isoform 4).
/FIId=VSP 004116. (in isoform 3 and isoform 4). Length 2845; 145CA73CF570A499 CRC64; LEU-RICH.
ARM 1.
ARM 2.
ARM 3.
ARM 4.
ARM 5.
ARM 5.
ARM 5.
ARM 5.
ARM 7.
SER-RICH.
ASP/GLU-RICH (ACIDIC).
ASP/GLU-RICH (ACIDIC). 90.2%; Score 13148; DB 1;

1019 IDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHVIEDEIKQNEGRQARSQNTSYPVYSE 1078	1260 CTYCVEDTPICFERGSSLSSLSSAEDBIGGNQTTQEADSANTLQIAEIKGKIGTRSAEDP 13	1379 ETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGGTMPPSRSKT 1438	1499 GFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNFTESEQFKESNENQEKEAEKTID 155	1557 1619 1617	1679 AQSGEPEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSH 1738 1677 IQGEFEKRDTIPTEGRSTDDAQGRCHISTOTPOLDDNKAEEGDILAECINSAMPKGKSH 1736 1739 KPFRYKKIMDQVQAASSSSAPNKQLDGKKKKFTSPVKNTBPRTRTRTRTRTRTRTRTRTRTRTRTRTRTRTRTRTRTR	1799 LNAERVFSDNKDSKKQNLKANSKDFNDKLPNNEDRVRGSPAFDSPHHYTPIEGTPYCFSR 185 : 1797 VNTEETFSDNKDSKKPSLQTNAKAFNEKLPNNEDRVRGTFALDSPHHYTPIEGTPYCFSR 185	1859 1857 1919	1917 NRAQSKPVLQKQPTFPQSSKDGPDRGAATDEKLQNLAIENTPVCFSRNSSLSSLSDIDQE 1	1977 2038	2098
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Best Local Similarity 90.0%; Pred. No. 0; Matches 2566; Conservative 113; Mismatches 159; Indels 12; Gaps 10; Conservative 113; Mismatches 159; Indels 12; Gaps 10; Mahaasydollkovalkmensnirgelednsnhirkleteasnmkevlkologsiedeam 60	119 RIFVNGSRESTOYLEELEKERSLLLANLDKEEKEKMYYAQUQNLITKRIDSLPLITENFSL 177 181 QTDLTRRQLEYEARQIRVAMEEQLGTCQMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 24/	301 PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQUSFALKVDHEIASVLDSSSGIASA 29 301 PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 36 299 PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 35 361 HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLEDIRAYCETC 42	359 HGNDKDSVLLGNSKGSKEARARASAALHNIIHSQPDDKKGKKEIKVLHLLEQIRAYCEIC 418 QY 421 WEWQEAHEPGMDQDKNPWPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ 480 DD 419 WEWQEAHEQGMDQDKNPWPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ 478 QY 481 VDCEMYGLTURRYAGMALTNIFFGDVANKATLCSWKGCMRALVAQLKSESEDL 540	DD 479 VDCEMYGLTNDHYSTATINGTHINGTHINGTHINGTHINGTHINGTHINGTHINGT	601 ENKADICAVDALAFLYGTLTYRSQTNTLAIIESGGGILRNYSSLIATNEDHRQILRENN 66	Db 659 CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM 718 Qy 721 GSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS 780	OY 781 PKASHRSKQRHKQSLYGDXVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS 840 	841 LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLOISTTAAQIAKVMEBVSAIHTS 90	OF COMPANY CONTROL	DD 959 NDSLNSVISSDGYGKRGQMKPSVESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE 1018 QY 1021 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDBIKQSEQRQSRUSTTYPVYTE 1080

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                    KPFTSNKGPRILKPGEKSTLEAKKIESENKGIKGGKKVVKSLITGKIRSNSEISSOMKOP
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                                                                                                                                                                                                                                                YNDGRPTKRHDIARSHSESPSRLPINRAGTWKREHSKHSSSLPRVSTWRRTGSSSSILSA
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                                                       SVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGI
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                                                                                                                                                                                                                                                                                                                                                                 SPIVERTPESSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNT
                                              LQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGOTATTSPRGAKP
                                                                                                                                                            ASKGINQMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKL
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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-!- FUNCTION: Structural protein involved in the filamentous cross-
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MEDLINE=92355629; PubMed=1379599;
Langkopf A., Hammarback J.A., Mueller R., Vallee R.B., Garner C.C.
"Microtubule-associated proteins 1A and LC2. Two proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    KKRDSKTDITESSGAQSPKRHSGSYLVTSV 2845
                                                                                                                                                                                                                                                                                                                                                                                                                                2814 KKRDSKTDSTESSGTQSPKRHSGSYLVTSV 2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -----EDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWD 700
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bridging between microtubules and other skeletal elements.
-!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAPIA and MAPIB proteins.
-! TISSUE SPECIFICITY: BRAIN, HEART AND MUSCLE.
-!- DEVELOPMENTAL STRAGE: EXPRESSED LATE DURING NEURONAL DEVELOPMENT APPEARING WHEN AXONS AND DENDRITES BEGIN TO SOLIDIFY AND STABILIZE
                                                                                                                                                                                   DOMAIN: THe basic region containing the repeats may be responsible for the binding of MAPIA to microthubules.

PTM: Various serine residues may be phosphorylated by CAMP kinase. PTM: LC2 IS COEXPRESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FORM MAPIA BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH SIMILARITY: TO MAPIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ----RNVSSLIATN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MAPI LIGHT CHAIN LC2.
LYS-RICH (BASIC).
11 X 3 AA REPEATS OF K-K-[DE].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      299526 MW; 3DEF74427BA9D7D7 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3.3%; Score 477; DB 1;
18.7%; Pred. No. 2.4e~10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                609 VDGALAFLVGTLTYRSQT----NTLAIIE--SGGGIL-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          57 GFNILVDGGSDRK-----SCFWKLVRHL----
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2774 AA;
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Best Local Similarity
Matches 542; Conserv
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424
424
427
431
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CHAIN ?24
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ENNN-KENEPI---KETEPPDSQGEP-- 1999 KKIMDOVQQASASSAPNKNQLDGKKKKP 1772 FSDNKDSKKQNLKONSKDFNDKLENNED 1832 PKPILQKQSTFPQSSKDIPDRGAA--- 1946 SLSSLSIDSEDDLLQECI-SSAMPK--K 2050 ILSLKSGISLGSPFHLTPDQEEK----P 2158 TESTAPMRNEPTTPSWLAEIPPWVPKDR 1816 YDSVVAAVQEGAAELEGGPYSPLGKDYR 1876 | TRDTEQTEPEQREPTPYPDERSFOYADI 1936 ELSPVAROTSQIGGSSKAPSRSGSRDST 2308 : KEEAAGCNTSAEKETSSPASPQNLQSDT 1996 PG------RNGISPPNKLSQLPRT 2348 PPAVPPRAPISLSKDLSPPLNGSTVSCS 2054 EGLGSGKESAAHSLWDLTP--LSPA--- 2278 EHSKHSSSLP-----RVSTWRR 2566 | :|: | : : KDLDREDQGQRAGPPABKDKASEQRDTD 1428 LDFDDDDVDLSREKAELRKAKE---NKE 1889 TDDKEQKEEASEEKEQVLEQKDWALGKE 1521 KKSLITGKVRSNSFISGOMKOPLOANMP 2222 T----- PASKSPSE----- 2263 OTGLSKNASSIPRSESASKGLNO---MN 2405 AFGFSSLQPAPPQLPSPAEPRSAPCGSL 2163 RRKLEESASFES----LSPSSRPASP- 2474 VQAGG------WRKLPPNLSPTIEY 2517 -----GLPGDLGDGTLPCRPECTGEL 2318 SGTKQSKENOVS---AKGTWRKIKENEF 2620 DLTLDLKDIQRPDSEHGLSPDSENFDWK 2102 ILETKKIESESK------ 2186 DSDĽEKGÁREQPEKÉTRŠPSPHHPMPMG 2103

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[8]
FUNCTION
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TKKPSPFLSPSGD--HEANGPGETSLNPPGFVTATAEKEEAEAPHAWERGSWPEGAEKSS 2376
                                                                                                                                                         2709
                                                                                                                                                                                                                                                  2710 SVPMRTVGLENRLTS-----FIQVD-APDQKGT-BIKPGQN-NPVPVSETNESP---IV 2757
                                                                                               2655 EDVWVRIEDCPI----NNPRSGR-SPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNG
                                                                                                                                                                                                    2437 DDSDLSTEEARLAGKGGRRRVGRPGATGGPCPMAD---ETPPTSASDSGSSQSDSDVPPE
                                                                                                                                                                                                                                                                                          2494 TEECPSITAEAALDSDEDGDFLPVDKAGGVSGTHHPRPGHDPPFTPLPDPRPSPPRPDVC
                                                                                                                                                                                                                                                                                                                                          2758 ERTPFSSSSSS-----KHSSPSGTVAARVTPFN-----YNPSPRKSSADSTS-
                                                                   --------APAVSKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. (ISOFORMS 3 AND 4), FUNCTION, ALTERNATIVE PROMOTER USAGE, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTANTS B9 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Embryo;
MEDLINE=20157049; PubMed=10655223;
Rebay I., Chen F., Hsiao F., Kolodziej P.A., Kuang B.H., Laverty T., Suh C., Voas M., Williams A., Rubin G.M.;
"A genetic screen for novel components of the Ras/mitogen-activated protein kinase signaling pathway that interact with the yan gene of Drosophila identifies split ends, a new RNA recognition motif-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20025936; PubMed=10556062; Mace K.A., Ronshaugen M.R., Wang F.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "spen encodes an RNP motif protein that interacts with Hox pathways to repress the development of head-like sclerites in the Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1), SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Neoptera, Endopter-Ygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                                                                   2621 SPTN--STSQTVSSGAINGAESKTLIYQM-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPEN DROME STANDARD; PRT; 5560 AA. 088X83; 09NHN1; 09NJ7; 09U6C3; 09VPL1; 09VPL2; 10-0CT-2003 (Rel. 42, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2614 TVPRPRSTPSQVTSAEEK 2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Jevelopment 126:5373-5385(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                   --ARPSOIPTPVNNNTKK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            containing protein.";
Genetics 154:695-712(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Split ends protein.
SPEN OR CG18497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WCBI_TaxID=7227;
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                                                                                             FUNCTION ON WG PATHWAY.

MEDLINE=22668876; PubMed=12783785;

Lin H.V., Dorroquez D.B., Cho S., Chen F., Rebay I., Cadigan K.M.;

"Splits ends is a tissue/promoter specific regulator of Wingless signaling.";

Development 130:13125-1335(2003).

-! FUNCTION: Probable corepressor protein, which regulates different key pathways such as the EGF receptor and Wg pathways. Involved in neuronal cell fate, survival and axon guidance, cell cycle regulation and repression of head identity in the embryonic trunk. May act with the Hox gene Deformed and the EGF receptor signaling pathway. Positive regulator of the Wg pathway in larval tissues but not in embryonic tissues. May act as a transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Isold=Q86X83-4; Sequence=vSP_008565, VSP_008566, VSP_008567; NOGe=Produced by alternative splicing of isoform 2; TISSUE SPECIFICITY: Ubjuitous. Expressed prior to callularization in stage 3 embryos, and in blastoderm cells, including pole cells. Expressed throughout the rest of embryogenesis. Later, it is expressed at higher level in epidermal cells and CNS. DEVELOPMENTAL STAGE: Isoform 3 is expressed both maternally and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          zygotically.
--- SIMILARITY: Belongs to the Spen family.
--- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
---- SIMILARITY: Contains 1 SPOC domain.
--- CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
                                                                                                                                                                                                                                                                                                                                                                                                                   proteins.
SUBCELLULAR LOCATION: Nuclear.
ALTERALIVE PRODUCTS:
Event-Alternative promoter;
Comment-2 isoforms, 1 (shown here) and 2, are produced by use
                   "split ends, a new component of the Drosophila EGF receptor pathway, regulates development of midline glial cells.";
Curr. Biol. 10:943-946(2000).
                                                                                                                                                                                                                                                                                                                                                                              corepressor protein, which repress transcription via the recruitment of large complexes containing histone deacetylase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=3; Synonyms=Spent;
ISOId=QBSXB3-3; Sequence=VSP_008567;
Note=Produced by alternative splicing of isoform 1;
Name=4; Synonyms=SpenS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IsoId=Q85X83-2; Sequence=VSP_008565, VSP_008
Note=No experimental confirmation available;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alternative promoters;
Event=Alternative splicing; Named isoforms=4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q8SX83-1; Sequence=Displayed;
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FlyBase, FBGM0016977; spen.
GO, GO:0007411; P:axon guidance, IMP.
GO, GO:0008347; P:glia cell migration;
InterPro; IPR00504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL, AF188205, AAF13218.1; --
EMBL, AF184612, AAF26299.1; --
EMBL, AF221715, AAF74661.1; ALT_INIT.
EMBL, AE003590, AAF51534.2; --
EMBL, AE003590, AAF71535.2; --
EMBL, AE003590, AAF71511; --
EMBL, AE003590, AAM10511.1; --
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SMART; SM00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
Rebay I.;
                 "split end
regulates
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1997 DKEQKEKEIREKDIREKEQRERDNREKELRDKDLREKEMREKEQREKELHREKDQREREH 2056
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                                                                                                                                                                                                                                                    2 AAASYDQLLKQVE---ALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIBDE
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                                                                                                                                                            Query Match
3.3%; scure 1.1.7,
Best Local Similarity 18.2%; Pred. No. 6.5e-10;
Matches 640; Conservative 498; Mismatches 1307; Indels 1065;
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PROSITE; PS50917; SPOC; 1.
Transcription requiation; Repressor; Developmental Nuclear protein; Repeat; RNA-binding; Coiled coil; Alternative promoter usage; Alternative splicing. DOWAIN 554 632 RNA-BINDING (RRM) 1. DOWAIN 656 730 RNA-BINDING (RRM) 2. DOWAIN 734 806 RNA-BINDING (RRM) 2.
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>-	1662	IESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSS 1707
٥	3553	ISSCSNISABASAIASASASISFGSPIASQNAMPQASIPKÇGPIİPQ-ÇAIRTQSLIMQPP 3611
>-	1708	CINSAMPKG
۵	3612	TISIPEQTPHFAVPQWLSPCSHHPQQPGTYWGIRAPSPHSPLHSPGRQV 3662
>-	16	-AERVFSDNKD 181
Ω	99	QQVQQTQQQHALITSPQSSNISPLASPTTRVLS-SSN 372
> -	81	KKQNLKNNSKDFNDKLPNNED 184 KKQNLKNNSKDFNDKLPNNED 184
Ω	72	PTTSKVNSYOPRNQQVPQQPSPKSVAEVQTTPQLMTIPLQKMTPIQVPHHPIIISKVVT 37
>- 1	1848	PIEGTPYCESRNDSLSSLDFDDDDVDLSREKAELKAAKNKESEAKVISH 1897
· >	0 0	NOOSANKTQAI 191
ڡ	3833	
>-	1914	AKQPINRGQPKPILQKQSTFPQSSKDIPDRGA 1945
۵	3893	GHPTQKQHQAQQQFNQQIQQHQSQQQHQVQQQNAQAQQQHLSQQQHQSQQQLNQQHQ 3949
>-	1946	ATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPD- 1994
۵	3950	AQQQQLQQLQXLQQMHGPQQQQXSPQGVGHLGGSTSIFASQQHNSQLFARGVPQQQHPQQ 4009
>-	1995	KSFHVED
۵	4010	LSHSSPCKPNTLVSVNQGVQPPAILTRVGSHSQPNQQQQLPHQQSSSGHP 4059
>-	2049	KKKKRSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAI 2104
۵	4060	HQKQLSSPGANLPLQTPLNVIQNTPKİIVQQHIVAQNQVPPPQTQGNAIHYPQN 4113
	2105	TPDQE 2
۵	4114	-QGKDSTPPGHVEPTPAMSAQKTSESVSVIRTPTTGLAVISANTVGS 4161
ب	2156	KPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISG 221
۵	4162	LLTBENLIKISQPKQDELIEQDSKEVDSDYWSAKEVNIDSVIKKLDTPLASKDAKRAV 4219
> 1	2212	OMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPA 2257
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>	2316	PLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSS 2359
. ۵	4331	QQLDIQRK
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۵	4387	
>-	2420	SSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQA 2479
Ω	4437	PKTISSVAPSABDQRPRLILTINKTQPSIKNISBMEQTIQQQQQQ 4481
>-	2480	253
Д	4482	QSEVISNTDPIGGDNSESCNTRKSRRLQEKEDRSTVDDIIEDVVRNTNTPTG1GPH 4537

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4823 QQ------QPPQ-IVAPAKQPIILQQNPLPTVLHHAQHTTVRPPQPLKAHVLNRE 4870
                                             4596 TVAASHLAPPEGAGVESHVPQLDAKEVEPVSVVTPISTPAPVSVAAPVTVPVPAMVPVKP 4655
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TISSUE-Liver, and Pituitary;
MEDINE-2131199; PubMed-11331609;
Shi Y., Downes M., Xie W., Kao H.-Y., Ordentlich P., Tsai C.-C., Hon M., Evans R.M.;
"Sharp, an inducible cofactor that integrates nuclear receptor repression and activation.";
Genes Dev. 15:1140-1151(2001).
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Q96758; Q9H9A8; Q9NWH5; Q9UQ01; Q9Y556;
10-0CT-2003 (Rel. 42, created)
110-0CT-2003 (Rel. 42, Last sequence update)
110-0CT-2003 (Rel. 42, Last sequence modate)
MSX2-interacting protein (SMART/HDAC1 associated repressor protein).
MINI OR STARP OR KIAA0929.
HOMO sapiens (Human).
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TISSUE-Embryo, and Teratocarcinoma;

ISOGAI T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Wakamatsu A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

"NEDO human cDNA sequencing project.";

Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryofa, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NOBI_TaxID=9606;
                                                                                                                               SILSASSESSEKAKSE ---- DEXHVNSISGT -----
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Rhodes S., Huckle E.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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2533 SESPSRLPINRSGTWKREHSKHSSSL-
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MEDLINE-97237633, PubMed-9119401;
Crozet F., El-Amraoui A., Blanchard S., Lenoir M., Ripoll C., Vago P.,
Hamel C., Fizames C., Levi-Acobas F., Depetris D., Mattei M.-G.,
Weil D., Pujol R., Pettit C.,
"Cloning of the genes encoding two murine and human cochlear
unconventional type I myosins.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 1-112 FROM N.A.

Adachi J., Alzawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Adachi J., Alzawa K., Akimura T., Hori F., Imotani K., Hashizume W., Hayashida K., Hirozane T., Hori F., Imotani K., Hashizume W., Mayazaki M., Kayama Y., Kodno S., Konno H., Koya S., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Ohsato N., Saito R., Salazume N., Sano H., Sasaki D., Sato K., Shibata K., Shiraki T., Tagami M., Takeda Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y., Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Brain,
TISSUE=Brain,
MEDLINE=22579291; PubMed=12693553;
MEDLINE=22579291; PubMed=12693553;
MEDLINE=22579291; PubMed=12693553;
MAKAjima D., Nagase T., Ohara R., Inamoto S., Aizawa H., Yuasa S.,
Nakajima D., Nagase T., Ohara O., Koga H.;
Prediction of the coding sequences of mouse homologues of KIAA gene:
II. The complete nucleotide sequences of 400 mouse KIAA-homologous
cDNAs identified by screening of terminal sequences of cDNA clones
randomly sampled from size-fractionated libraries.";
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MEDLINE=22261914; PubMed=12374742;
Oswald F., Kostezka U., Astrahantseff K., Bourteele S., Dillinger K.,
Zechner U., Ludwig L., Wilda M., Hameister H., Knoechel W., Liptay S.,
Schmid R.M.;
"SHARP is a novel component of the Notch/RBP-Jkappa signalling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EQUENCE OF 69-3644 FROM N.A. (ISOFORM 2), AND VARIANTS THR-348; PHE-762; PHE-773 AND LEU-933.
STRAIN=ICR; TISSUE-Brain;
Sakamoto T., Gotou T., Isagawa Y., Mimura H., Kimura K., Kawaichi M.;
J/Suff) activity.
Sylan negatively regulates Notch signaling by inhibiting RBP-3/Suff) activity.
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 49-3644 FROM N.A. (ISOFORM 1), FUNCTION, SUBCELLULAR SEQUENCE OF 49-3644 FROM N.A. (ISOFORM 1), FUNCTION, TISSUE SPECIFICITY, DNA-BINDING, AND INTERACTION WITH MSX2. ISSUE=FESTIS; MEMBERS E.P., Latifit T., TOWLER D.A.; Newberry E.P., Latifit T., TOWLER D.A.; Newberry E.P., Latifit T., TOWLER D.A.; "The RRM domain of MINIOR DEPOSIT SET A movel mSX2 binding protein, recognizes and regulates the rat osteocalcin promoter."; Biochemistry 38:10678-10690(1999).
                                                                                                                                         MINIT MOUSE STANDARD; PRT; 3644 AA.
062504; Q80TN9; Q99P84; Q90ZW2;
10-0CT-2003 (Rel. 42, Lreated)
110-0CT-2003 (Rel. 42, Last sequence update)
115-MAR-2004 (Rel. 43, Last annotation update)
MSAZ-1nteracting protein (SMART/HDAC1 associated repressor protein).
MINIT OR SHARP OR KIAA0929.
MNS musculus (Mouse)
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Mammalia, Eutheria, Rodentia, Sciurognathi; Muridae, Murinae, Mus.
1015_TaxID=10090;
                                1: | | 1 | 2440 VDEEPQARFRVHSIIESDPVTPP 2462
2809 VNNNTKKRDSKTDSTESSGTOSP 2831
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                                                                      R EMBL; BY726481; -; NOT ANNOTATED CDS.

R EMBL; AB55590; AAD55911; ALT_INIT.

EMBL; AB55590; BAB32766:1,

EMBL; Z78160; CAB01562.1; ALT_SEQ.

R EMBL; AR722402; BAG55684.2; ALT_SEQ.

R EMBL; AR722402; BAG5684.2; ALT_SEQ.

R EMBL; AR722402; RAG, NA_rec_mot.

R InterPro; 1PR000564; RNA_rec_mot.

R PETM; PR00076; RRM; 3.

R RAGSITE; PS50102; RRM; 4.

R PROSITE; PS50117; SPOG; 11.

R PROSITE; PS50117; SPOG; 11.

R PROSITE; PS50117; SPOG; 11.

R PROSITE; PS50117; SPOG; 11.

R PROSITE; PS50117; SPOG; 11.

R PROSITE; PS50117; SPOG; 11.

R PROSITE; PS50117; SPOG; 11.

R RNA-binding; Repeat; Colled coil; Alternative splicing; Polymorphism.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isoda-g62504-2; Sequence-vSP 008564,
Noce-No experimental confirmation available;
Noce-No Experimental confirmation available;
TISSUE SPECIFICITY: Highly expressed in testis. Expressed at lower level in brain, lung, spleen, liver and kidney. Weakly expressed in cardiac and skeletal muscles and ovary. In spleen, it is marginal zone B-cells, while it is weakly expressed in DOMAIN: The RID domain mediates the interaction with nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- DOWALN: The SPOC domain, which mediates the interaction with NCOR2, is essential for the repressive activity (By similarity).
-!- SIMILARITY: Belongs to the Spen family.
-!- SIMILARITY: Contains 1 RID (receptor interacting) domain.
-!- SIMILARITY: Contains 1 RID (receptor interacting) domain.
-!- SIMILARITY: Contains 1 SPOC domain.
-!- CAUTION: Ref. 4 sequence differs from that shown due to multiple frameshifts and conflicts that create stop codons.
-!- CAUTION: Ref. 5 sequence differs from that shown due to what seems to be the presence of intronic sequence in the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q62504-1; Sequence=Displayed;
                                                               MEDLINE=22483652; PubMed=12594956;
                                            FUNCTION, AND TISSUE SPECIFICITY
pathway.";
EMBO J. 21:5417-5426(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptors.
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SSTASDDSPAR------SVQSAAVPAPTSQLLSSLEKDEPRKSFGIK 339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  400 KLFFGMQIEVTAWVGPETESENEFRPLDERIDEFHPKATRTLFIGNLEKTTTYHDLRNIF 459
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          727 RNLMANRPAK-YKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLSPK--A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3.0%; Score 434.5; DB 1; Length 3644; ilarity 18.7%; Pred. No. 1.2e-08; Conservative 321; Mismatches 894; Indels 1069;
DNA-BINDING.
RAA-BINDING (RRM) 1.
RNA-BINDING (RRM) 3.
RNA-BINDING (RRM) 3.
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WITH RBPSUH.
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/FTId=VSP_008564.
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OEO OEO ANDENDENDENDENDENDENDENDENDENDENDENDENDEN	QREGEIVDIDIKKVNGVPQYAFLQYCDIASVCKAIKKMGGEYLGNNRLKLGFGKSMP	982 SIESYSEDDESKFCSYGOYPADLAHKIHSAN	: : : :	1013 HMDDNGGELDTPINYSLKXSDEQLNSGRQSPSQNERWARP 1013 HMDDNGGELDTPINYSLKXSDEQLNSGRQSPSQNERWARP 1013 HMDDNGGELDTPINYSLKXSDEQLNSGRQSPSQNERWARP 1013 HMDDNGGELD			1106 GANGSETNRVGSNHGINONVSQSLCQEDDYEDDKPINYSERYSEE	678 GREFYSEWETYQGEYYDSRYYDEPREYREYRSDEYEQDIREYSYR	EQHEEEERPINYS	723 QRERERERERERFESDRDHERRPIERSQSPVHLRRPQSPGVSPAHSERLPSDSERRL	1195 FSPSKSSSQQSSKSS	778 YRRSSERSGSCSSVSPPRYDKLEKARLERYTKNEKADKËRTFDPERVERERRIVRKEKGE	1224 NAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSA	838 KDKAERQKRKGKAHSPSSQPSETEQENDREQSPEKPRG	1284 EDEIGCNQTTQEADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRL	876 STKLSRDRADKEGPAKNRLELVPCVVLTRVKEKEGKVIEHPPPEKLKARLGRDTTKASAL	1338AQSSLSSESARHKAVEFPSGAKSPSKGGAQTP	936 DQKPQAAQGEPAKSDPARGKALREKVLPSHAEVGEKEGRTKLRKHLKAEQTPELSALDLE	1370	996 KLEARKRRFADSGLKIEKQKPEIKKTSPETEDTRILLKKQPDTSRDGVLLREGESERK	1387CTSVSSLDSFESRSIASSVQSEPGSGMVSGIISPSDLPDSP	1054 PVRKEILKRESKKTKLERLNSALSPKDCQDPAAVSAGSGSRPSSDVHAGLGELTHGS	GOTMPPSRSKTPPPPPQTAQTKREVPKUKAPTABKRESGPKQAAVNAAVQRVQVLPDAD 	1111 VETQETQPKKAIPSKPQPKQLQLLENQGPBKEEVRKNYCRPREEP		1		VARKPSQLPVYKLLPSQNRLQPQ-KHVSF	1241 KKRRIDHVD-FDICIKRERNYRSSRQISEDSERISCSPSVRHGSFHDDDDFRGSPRLVSV	1645 EGTPINFSTATSLSDLTIESP	1300 KGSPKGDEKGLPYPNAAVRDDPLKCNPYDSGKREQTADTAKÍKLSVLNSEGEPSRWDPPM	1666PNELAAGEGVRGGAQSGEFEKRDIPTEGKS-TDEAQGGKTSS- : :	VIIPELDDNKAEEGDILA	
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EMBL, 136825; AAA98810.1; JOINED.
EMBL, 136826; AAA98810.1; JOINED.
EMBL, 136827; AAA98810.1; JOINED.
EMBL, 136827; AAA98810.1; JOINED.
EMBL, X68946; CAA4876.1; JOINED.
EMBL, X68946; CAA4876.1; JOINED.
EMBL, X68946; CAA4876.1; JOINED.
EMBL, X68946; TAA98810.1; JOINED.
EMBL, X68946; TAA98810.1; JOINED.
EMBL, Y68947; ISA477.

FIGHT, FORDORY, ZIF, C2H2.
EMML, PF00096; ZF-C2H2; S.
SMART; SM00355; ZF-C2H2; S.
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      AAA98810.1;
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2418 KTPCKAPVLPALPPLSQPAL-MDDGPQARPKVHSIIESDPVTPPSDSGIPPPTIPLVTIA 2476
                                                                                         2526
                                                                                                                                                                                                                                                            -------PPLEGVSAAAVPN----ADTQASEVPVAAD 2603
                                                                                                                                                                                                                                                                                                       2703 KONVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPF 2762
                                                                                                                                                                                                                                                                                                                                                2604 KEKVAPVIAP-----KITSVI-----SRMPVSIDLENSOKITLAKPA 2640
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                                                                                    2477 KLPPPVIPGGV-----PHOSPPPKVTEWITRQEEPRAQSTPSPALPPDTKASDMD----
                                                                                                                                                                         ----TSSSTLRKILMDPKYVSATGVTSTSVTTAIAEPVSAPCL---QEAPA
                                                                                                                                                                                                                  2651 VSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQA-----
                                                                                                                              2593 NSISGTKOSKENOVSAKGTWRKI--KENEFSPTNSTSQTVSSGATNGAESKTLIYQMAPA
                                             RL--PINRSGTWKREHSKHSSSLPRVSTW---RRTGSSSSILSASSESSEKAKSEDEKHV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nakamura T., Donovan D.M., Hamada K., Sax C.M., Norman B., Flanagan J.R., Ozato K., Westphal H., Piatigorsky J., "Regulation of the mouse alpha A-crystallin gene: isolation of a cDNA encoding a protein that binds to a cis sequence motif shared with the major histocompatibility complex class I gene and other genes."; Mol. Cell. Biol. 10:3700-3708(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Transcription factor alphaA-CRYBP1) (Alpha A-CRYSTAILIn-binding protein I) (Alpha A-CRYBP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- SUBCELLULAR LOCATION: Nuclear.
-!- DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY SEPRATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH ZINC-FINGER IN-BETWERN.
-!- SIMILARITY: STRONG, TO HIVEP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: TRANSCRIPTION FACTOR WHICH BINDS SPECIFICALLY TO THE PALINDROMIC SEQUENCE 5'-GGGAAATCCC-3' IN THE ALPHA-A CRYSTALLIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Brady J.P., Kantorow M., Sax C.M., Donovan D.M., Piatigorsky J., "Murine transcription factor alpha A-crystallin binding protein I Complete sequence, gene structure, expression, and functional inhibition via antisense RNA.";
                                                                                                                                                                                                                                                                                                                                                                                          2763 SSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSOIPTPVN 2810
                                                                                                                                                                                                                                                                                                                                                                                                                                   2641 POTLIGLVSALIGLVNVSLVPVNALKGPVKGSVATLKGLVSTPAGPVN 2688
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TISSUE-Lens epithelium;
MEDLINE-90287161; PubMed-1694016;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       230 VRSPSKLKNSSLDAPNATSPDLVVESPCPPCTSYPVHVASTQKSEQVAAQCVSHLYSSQD
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PROSITE; PSO1028; ZINC FINGER C2H2 1; 4.
PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.
Transcription regulation; Zinc-finger; Metal-binding; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 2688;
                                                                                                                                                                                                                                                                                                                                                                                                             288341 MW; SEAD46C3A7008BE6 CRC64;
                                                                                                                                                                                                                                                                 (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 18.4%; Pred. No. 3.7e-08;
Matches 463; Conservative 323; Mismatches 898;
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Pred. No. 3.7e-08;
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Mammalia; Butheria; Primates; Catarrhini; Homin NCBI_TaxID=9606;	OX		296	2253 LKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSS 2296	Qy dq
(Human). etazoa; Chordata;	O O O	;	514	::: : : saddearth.com.	qq
18-001-2001 (Net. 40, mask ammoration update) Microtubule -associated protein 1A (MAP 1A) (Pro- protein p80) (Contains: MAP1 light chain LC2).	1 E E		v 6	1401 GIAHVELLEKKKGFLIKQISLNIASUSALSFGSAAALQIIVLESVNI-VFKQAFKLEVNA 1459 2200 TGKVRSNSEISGQMKQPLQANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPP 2252	8 8
15-UU1-1998 (Rel. 36, Created) 16-OCT - 2001 (Rel. 40, Last sequence update)	122		6 (NKGPRIKPGEKSTLETKKIESESKGIKGGKKVYKSLI	ठे ह
MARA HUMAN STANDARD; PRT; 2805 AA. 20 DARREY, OSK643, O12973, O15882, OSTITT4.	MAPA		į 0		3 8
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2317 SSVGLPPAVAGLNPQPAARISSSVSPHPDSQDKQQII	g		ω Ο	20//	දු අ
2797 STSARPSQIPTPVNNNTKKRDSKTDSTESS	ò		٠ -	SHDEEKSEKFTWPQRSETLSKLFTEKLFPKKKRLRLAELEHSSTESSFESTLSRSLSRES	au ,
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	ò i		0	1996QGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSL 2030	ò
2148 SDEKQRFGCERSGYDLEESDGPDEDDNDNEEDDDD	ф		ŭ ,	124 OHTWSLENDIDORNNNKENERI	ž 8
2662 EDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKD	ģ		m	RGVQLVARGP-ERALPLKQCPMVEQQLINAAAQDKMEVKRQGGGISVI	අධ
Z615 IKENEESPINSISOLASKAN CARE	දි දි		m	NKTQAIAKQPINRGQPKPILQKQ-STFPQSSKDIPDRGAATDEKLQNFAIENTPVCF	δλ
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2581 SEKAKSEDEKHVNSISGTKOSKENOVSA	δ		7 -	958 CRNKYRKLENFENHKKFYCSELHGPKTKAAVREAEHGPAPGGAQPQVLHYRVAAPTAVWE 1017	යි දි
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2528 IARSHSESPSRLPINRSGTW	ò		w	85Z FPFSLKGSQSFDDKIGTLYDVVGAAV 897 1756 SSSAPNROOLDGKKKKTTSPVKPIPONTEXRTRVRKNADSKNNLNAERVFS 180	8 8
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1799 LEQGACSASGRSSNKAANLTQVLPTDSL	දු දි			: :	QQ .
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1743 AMEKHQKRAKDENGAVCSTNIRALELPSSRANESHKQK	qq		on on	1616 KLLPSQUKLQPQKHV-8FTPGDDMRVVCVEGTPINFSTATSLSD 165 : : : : : : : :	Š 8
2398SKGLNQMNNGNGANKKVELSRMSSTKSSGSESDRSE	ò			TPFARTFPTMDPDPAKNGGAPGPRISAPAPSALATGEKSSVVTGQMRPPLATKTLEERIS 74	Dp
25/1 KONGOGLINALGENESSIA	6 6		ហ		δ
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SERPULVRQSTFIKEAPSPTLRRK 2455
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?KKPVLVRQLC---TTEPLEGAA 1798 SLSTHSS------VQAGGWR 2505 ABSKTLIYQMAPAVSKTEDVWVRI 2661 .: | : | ... RISPQQESSASSKRMLSPANSLDI 1742 | ||: PGVRHEENKVIQGQRPPLVSGLSL 1908 :::: |:: WKUNLSKRALGNQKATVVEFSNKD 2028 YVRGRGRGKYICEECGIRCKKPSM 2088 KDNQAKQNVG----- 2707 -PLELGL-PRDEVLQKQLPSFVL 1622 -----KSSGSGKMSYTSPG 2370 KREHSKH----SSSLPR---- 2560 :: | : | | | | | | | OKTSAYTGWTVSSSNPNPLGLPT 1968 -----SSILSASSES 2580 |:||: |SOSQAESGLSAAPSVTASPQHLPS 2204 ILLOPPGGLPSPKRHSGSYL 2839 PAKRHD----roliferation-related brata; Euteleostomi; inidae; Homo. us-09-442-489f-2.rsp

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The stanta representation of human microtubule-associated protein IA "Brain-specific expression of human chromosome 15.";

(MAPLA) gene and its assignment to human chromosome 15.";

U. Neurosci. Res. 40:820-825(1995).

-!- FUNCTION: Structural protein involved in the filamentous cross-bridging between microtubules and other skeletal elements.

-!- SUBUNIT: 3 different light chains, LCI, LC2 and LC3, can associate with MAPLA and MAPLB proteins.

-!- SUBUNIT: 3 different light chains, LCI, LC2 and LC3, can associate with MAPLA and MAPLB proteins.

-!- DOMAIN: THe basic region containing the repeats may be responsible containing of MAPLA to microtubules.

-!- DOMAIN: THe basic region containing the phosphorylated by CAMP kinase.

-!- PTM: LC2 IS COEXPRESSED WITH MAPLA. IT IS A POLYPEPTIDE GENERATED READ MAPLA AND MAPLB.

-!- PTM: LC2 IS COEXPRESSED WITH MAPLA. IT IS A POLYPEPTIDE GENERATED READ MAPLA AND MAPLB.

-!- SIMILARITY: TO MAPLB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FWBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
                                                                                            TISSUE-Ovarian carcinoma;
Chen Z.C., Faddel A., Naftolin F.;
"Identification of a novel protein (P80) in ovarian carcinoma cells.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
Fink J.K., Jones S.M., Esposito C., Wilkowski J.; "Human microtubule-associated protein la (MAPIA) gene: genomic organization, cDNA sequence, and developmental- and tissue-specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Brain;
Ohtani K., Rutherford T., Sakamoto H., Naftolin F.;
Microtubule associated protein IA (MAPIA) in human brain -
sequence and physiological role.";
Submitted (NOV-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                            SEQUENCE OF 134-419 FROM N.A.
TISSUE=Fetal muscle;
Chiannilkulchai N., Pasturaud P., Richard I., Auffray C.
                                                                                                                                                                                                                                                                                                                   Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GO; GO:0005875; C:microtubule associated complex; TAS. Microtubule; Repeat; Phosphorylation 2249
                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain;
MEDLINE=95356255; PubMed=7629894;
                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 1607-1883 FROM N.A.
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EMBL; U38292; AAB41133.1; -.
EMBL; AF200415; AAF08305.2; -.
EMBL; Z47038; CAA87104.1; -.
EMBL; U14577; AAA81362.1; -.
                                                                                                                                                               SEQUENCE OF 78-1687 FROM N.A.
                                                                                SEQUENCE OF 1-1825 FROM N.A.
                                                      Jenomics 35:577-585(1996).
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S -> G (IN REF. 4).
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306392 MW; F3ED0A3165993B2E CRC64;
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18.7%; Pred. No. 1.6e-07;
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1915 EREEEGRAEAPDK--SSHXSKVPEARKSHATTEPEQTEPEQREPTPYPDERSFQYADIYE 1972 2196 | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | 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RTGSSSSILSASSE---SSEKAKSEDEKHVNSISGT-------KQSKENQVSA 1890 -SEAKVISHTELISNQQSANKTQAIAKQPIN---RGQPKPILQKQSTFPQSS-----2414 VELSEMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFE-----2416 2367 2197 2247 1993 2166 2321 2464

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.7%; Score 400; DB 1; Le
Best Local Similarity 19.9%; Pred. No. 3.3e-07;
Matches 387; Conservative 243; Mismatches 765;
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  -----INNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKD 2699
                           2525 ITAEAALDSDEDGDFLPVDXXGGVSGTHHPRPPGHDP----PPL-----PQPDXRPS-- 2571
                                                                                                         2760 TPFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSK 2819
                                                                                                                                 2609 AP----GKDKPVSPXRRLXLR---GKRSPTPGKGSXDRVSRXPXRSRSXTSQVTPAEEKD 2661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        similarity).
                                                      2700 NQAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVER
                                                                              ------PPRP-----DVCMADPEGLSSESGRXERLRXKERVQGRVGRR
                                                                                                                                                                                                                                                                                                                                                  Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH RABACI.
MEDLINE-20170257; PubMed-10707984;
Fenster S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B.,
Garner A.M., Kaempf U., Kindler S., Gundelfinger E.D., Garner C.C.;
"Piccolo, a presynaptic zinc finger protein structurally related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21181819; PubMed=11285225;
Gerber S.H., Garcia J., Rizo J., Suedhof T.C.;
"An unusual C(2) -domain in the active-zone protein piccolo:
implications for Ca(2+) regulation of neurotransmitter release.";
EMBO J. 20:1605-1619(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -1- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity)
-1- SUBUNIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IsoId=Q90XS6-2; Sequence=VSP 003930, VSP 003931,
-!- DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fenster S.D., Cases-Langhoff C., Gundelfinger E.D., Garner C.C., Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CALICUM-BINDING ACTIVITY, AND MUTAGENESIS OF ASP-4668; ASP-4674; VAL-4688; MET-4689; VAL-4690; SER-4691; GLN-4692; ASN-4693 AND
                                                                                                                                                                                                                                                                  09JKŠ6; Q9JLT1;
28-FBB-2003 (Rel. 41, Created)
28-FBB-2003 (Rel. 41, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Piccolo protein (Multidomain presynaptic cytomatrix protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Event=Alternative splicing; Named isoforms=2;
                                                                                                                                                                                                                                                        5085 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=Q9JKS6-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Neuron 25:203-214 (2000).
                                                                                                                                                            2820 TDSTESSG 2827
                                                                                                                                                                                       2662 GHSPMSKG 2669
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                       PCLO_RAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     bassoon.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1299 ANTLOIAEIKGKIGTRSAEDPV---SEVPAVSQHPRTKSSRLQGS---SLSSESARHKAV 1352
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67 VPPAAABSPSMHRKQELDSSQAPQQPGKPPDPGRPTQPGLSKSRTTDTFRSEQKLPGRSP 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        QN->AA: MODERATE INCREASE IN AFFINITY FOR CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1187 IPSSOKOSFSFSKSSGOSSKTEHMSSSSENTSTPSSNAKRONOLHPS--SAQSRSGOPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VM->SS: 10-FOLD INCREASE IN AFFINITY FOR CALCIUM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STISLKESKSRIDFKEEYKSSMMPGFFSDVNPLSAVSVVNKFNPFDLISDSEASQEETT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OF
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RESEP: P04410; 1A25.

RESEP: P04410; 1A25.

RESEP: P04410; 1A25.

RESEP: P04410; 1A25.

RESEP: P04410; 1A25.

RESEP: P045202; C:synaptic junction; IDA.

RESEP: P045202; C:synaptic junction; IDA.

RESEP: P045202; C:sycoaptic junction; IDA.

RESEP: P045202; C:soldium dependent phospholipid binding; IDA.

RESEP: P0005522; F:profilin binding; ISS.

RESEP: P187034010; P:syraptic vesicle targeting in NaS.

RESEP: P187034010; P:synaptic vesicle targeting; NAS.

RESEP: P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P187034010; P1870340
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Missing (In isoform 2).
/FIId=VSP 003931.
D->A: COMPLETE LOSS OF CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          D->A: COMPLETE LCSS OF CALCIUM-BINDING
AND CALCIUM-DEPENDENT PHOSPHOLIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12 X 10 AA TANDEM APPROXIMATE REPEATS - PA-K-PO-P-Q-P-X. C4-TYPE (POTENTIAL). C4-TYPE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    M->S: INCREASED AFFINITY FOR CALCIUM.
VV->SS: 10-FOLD INCREASE IN AFFINITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          V->S: SMALL INCREASE IN AFFINITY FOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AND CALCIUM-DEPENDENT PHOSPHOLIPID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A->S: NO EFFECT ON CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels 546;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 5085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C2 DOMAIN 1.
C2 DOMAIN 2.
TKPIN -> SKRRK (in isoform 2).
/FIId=VSP 003930.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 5A1BB543201A7450 CRC64;
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Db 1191			DD 12/3 QY 2395	Db 1333	Qy 2453	Db 1377	Db 1426		Db 1481	Db 1540	Qy 2661	Db 1579		DD 1619	Qy 2//6 Db 1676	Oy 2812	Db 1736	SULT 11 K2_HUMAN		DT 01-APR-1 DT 01-OCT-1 DT 28-FEB-2	GN ANK2.				RT "Isolati RT ankyrins	RL J. Cell RN [2] RP REVISION	KA Carpente
																	-			,				- <u>i</u> i.	-		-
246 QAPGTGKPSQQSPAQTPAQQASPGKPVAQQPG 277	1413 MVSGIISPSDLPDSPGGTMPPSRSKTPPPPPQTAQTKREVPKNKAPTABKRESGPKQ 1469	AAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEFFIQKDVELR	330 LAQTPGHGKFPLGPVKSPAQQPGTAKHPAQQPGPQTAAKVPGP 372	1524 IMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSEKDLDDSDDDDI 1572	HILEBELI ISAMPTKSSRKGKKPAOTASKLPPPVARKPSOLPVYKLLPSONRL 16	:	1625 QPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQS 1681	GEFEKKDTIPTEGRSTDEAGGGKTSSVTIPELDDNKAEEGDI	LCNTTELLHIPEKANFNTCTECQSTVCSLCGFNFNPHLTEIKEWLCLNCQ	LAECINSAMPKGKSHKPFRVKKIMDQVQQASASSARNKNQLDGKK	585 AAAIPSSPQPTPKAATAPTATASKSPVPSQQASPKKEPPSKQDSPKALBSKKPPEPKKPP 644	1770KKPTSPVKP1778 	IPQNTEYRTRVRKAADSKANLNAERVFSDNKDSKKQNLKANSKDFNDKLPNNEDRV	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :		765TPLDSKAMPRPASDSKIISQPGPGSESKDPKHIDFIQKKDEPKKA-QP 811	1888 KESEAKVTSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSFFPQS 1936	SKDIPDRGAATDEKLONPALENTPVCFSHNSSLSSLSDLDQENNNKENEPIKETEPPD	870 QPTTPQETVTGKLFGFGASIFSQASNLISTAGQQGFHPQTGFAAPSKQAPTP 921	1995 SQGEPSKPQASGYAPKSFHVEDTPVCFGRNSSLSSLSIDSEDDLLQECISSAMPKKKK 2052	2053 PSRLKGDNEKHSPRNMGGILGEDLFLDLKDICRPDSEHGLSPDSENFDWKA 2103	978 PPPAKVGKPPPSEPEKAVPAHKPDKTTKPKPACPLCRTEINLG-SQEPPNFN-T 1029	2104 IQEGANSIVSSLHQAAAACLSRQASSDSDSILSLXSGISLGSPF 2148	2149HITPDOEEKPFTSNKGPRILKPGEKSTLETKKIESES 2185	1089 PAPAEPSSQKTPTGTQVKGKKKEAEGKTEAEKPVPEKETASIEKTPPMVTTDQKLEBSSE- 1147	2186 KGIKGGKKYYKSLITGKVRSNSEISGQMKQPLQNMPSISRGRTMIHIP 2234	
: 셤	& E	3 8	qq	හි සි	3 6	g Sp	8 8	3 8	. 원	ò	d d	Š É	} &	qq	λ̈́δ	qq	δ g	ζ	qq	ζ, dg	ò	QQ	& g	ò	QQ	& 43	

2512 2567 LNSTIADKYSSES-SQKKTILYFDEBPELEMESLTDSP--EDRSRGEGSSSLHASSFTPG 1675 TVAARVTPF--NYNPSPRKSSADSTSARPSQ-----IPT------PVNN 2811 6 TSPTSVSSLDEDSDSSSPSHKKGESKQQRKARHRSHGPLLPTIEDSSEEBELREEBELLKE 1735 E-SASKGINOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTL- 2452 GSSSS-----ILSASSESSEXAKSEDEKHVNS----ISGTKOSK 2602 ENQVSAKGTWRKI--KENEFSPINSTSQTVSSGAINGAESKTLIYQMAPAVSKTEDVWVR 2660 1 IEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNV---GNGSVPMRTVG 2717 2394 2235 GVRNSSSSTSPVSKKGPPLKTPASKSPSEGOTATTSPRGAKPSVKSELSPVARQTSQIGG 2294 LENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPFSSSSSSKHSS--PSG SSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTA STKSSGSGKWSY-----TSPGRQMSQQNLTKQTGLSKNA-----SSIPRS GSSKDGQGERSKEKTEKEEDKSDTSSSQQPKSPQGLSDTGYSSDGISGSLGEIPSLIPSD RRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLS GEKAEKKTQPQKISP-EKPQDQQKTQTASETL----DITIS-EEEIKESQEKK----VS PTIEYNDGRPAKRHDIARSHSESP---SRLPINRSGTWKREHSKHSSSLPRVSTWRRT-piens (Human). 12. Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, 12. Butheria, Primates, Catarrhini, Hominidae, Homo. 12. XTD=9606, Brain stem, >=91302466; PubMed=1830053; , Kunimoto M., McLaughlin T., Bennett V.; ion and characterization of cDNAs encoding human brain steveal a family of alternatively spliced genes."; Biol. 114:241-253(1991). MAN STANDARD; PRT; 3924 AA.
CO1485;
1993 (Rel. 25, Created)
1996 (Rel. 34, Last sequence update)
2003 (Rel. 41, Last annotation update)
2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid) E FROM N.A. (ISOFORMS 1; 2 AND 3). 6 QEKQRELEQQQRKSSSKKSKK 1756 2 NTKKRDSKTDSTESSGTOSPK 2832 STANDARD; 8

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EYKRSSND--SLNSVSSNDGYGKRG--QMKPSIESYSEDDESKFCSYGQYPADLAHKIHS 1010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1011 ANHMDDNDGELDTPINYSLKYSDEQLNSG-----RQSPSQ----NERWARPKHIIE 1057
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1564 DESIBEARQKAPLEITEYPC-VEVRIDKEIK-----GKVE----KDSTGLVNYLTDDLNT 1613
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1118 NHGINQNVSQSLCQEDDYEDDKPTNYSE-----RYSEEEQHEEEERPTNYSIKYNEEKRH 1172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1614 CVPLPKEQLQTV-----QDKAGKKCEALAVGRSSEKEGKDIPPDETQSTQKQHKPSLG 1666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1173 VDQPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLH 1232
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1667 IKKPVRRKLK-----EKÇKÇ------KEBGLQASAEKA------ELK 1696
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .233 PSSAQSRSGQ-----PQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEI 1287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        897 IHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSE--NSNRTCSMPYAKL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1421 IYTKESESDQEQEEBID-MISEKN-----DETESTETSVLKSHLVNEVPVLASPDLLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | ::: | | ::: | EVSEMKQDLIKMTAILTTDVSDKAGSIKVKELVKAAEEEPGEPF-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1517 -----EIVERVKEDLEKVNEILRSGTCTRDESSVQSSRSERGLVEBEWV----IVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1058 DEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative 307; Mismatches 799; Indels 658; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Missing (In isoform 2 and isoform 3).
/FIIdavSp 002088.
QQ -> PE [IN REF. 4).
I -> S (IN REF. 1).
QY -> HA (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.7%; Score 395; DB 1; Length 3924; 19.5%; Pred. No. 3.7e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     475 476 GQ -> PE TIN REF. 4).

971 J -> S (IN REF. 1).

3581 3582 QY -> HA (IN REF. 1).

3586 3586 J -> Y (IN REF. 1).

3924 AA, 430337 MW, 52AC496C426E29D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                           REPEAT A.
REPEAT A.
REPEAT A.
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REPEAT A.
  ANK 8.
ANK 9.
ANK 110.
ANK 111.
ANK 12.
ANK 13.
ANK 14.
ANK 15.
ANK 16.
ANK 16.
ANK 16.
ANK 21.
ANK 21.
ANK 22.
ANK 23.
ANK 23.
ANK 23.
ANK 23.
REPEAT-RICH REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (in isoform 2).
/FTId=VSP_000267.
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DEATH.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Isoid=001484-3; Sequence=VSP 000268;
-!-TISSUE SPECIFICITY: Plasma membrane of neurons as well as glial cells throughout the brain.
-!- PTM: Phosphorylated at multiple sites by different protein kinases and each phosphorylation event regulates the protein's structure and function (Potential).
-!- SIMILARITY: Contains 1 AnK repeats.
-!- SIMILARITY: Contains 1 death domain.
                                                                                                                                              regulated
                                                                                                                                                                                                                            SEQUENCE OF 463-495 FROM N.A.
MEDLINE=92009921; PubMed=1833308;
TSE W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                                                              Genomics 10:858-866(1991).
-!- FUNCTION: Attach integral membrane proteins to cytoskeletal elements. Also bind to cytoskeletal proteins.
-!- ALTERNATIVE PRODUCTS:
                                                                  TIŜSUE=Brain stem,
MEDLINE=94075409; PubMed=8253844;
Chan W., Kordeli E., Bennett V.;
440-kD ankyrinB: structure of the major developmentally redomain and selective localization in unmyelinated axons.";
J. Cell Biol. 123:1463-1473(1993).
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
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SWART; SM00005; DEATH; 1.
SWART; SM00218; ZUS; 1.
PROSITE; PSS0089; ANK REPEAT; 20.
PROSITE; PSS0017; DEATH DOMAIN; 1.
CYTOSKELECON; ALTERNATIVE SPLICING; Repeat; ANK repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=Q01484-1; Sequence=Displayed;
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EMBL; X56958; CAA40279.2; -.
EMBL; Z26694; CAB42644.1; -.
EMBL; M37123; AAA62828.1; -.
PIR; S37431; S37431.
HSSP; P42771; 1DC2.
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Interpro; IPR000488; Death.
Interpro; IPR000906; ZU5.
Pfam; PF00023; ank; 24.
Pfam; PF00023; death; 1.
Pfam; PF00791; ZU5; 1.
PRINTS; PR01415; ANKYRIN.
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MIM; 106410; -.
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Cell Biol. 147:151-162(1999)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUB-Placenta,

MEDLINE-22388257; PubMed=12477932;

A Straubberg R.L., Feligold B.A., Grouse L.H., Derge J.G.,

RIAURE-2188257; PubMed=12477932;

A Klauener R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hisleh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

B tapleton M., Soares M.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rowstein M.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

B Rosak S.A., McDwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Kichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Soderson B., Low, Gibbs R.A.,

Raha S.Y., Muzny D.M., Soderson M., Madan A., Rodriques S., Sanchez A.,

Rhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Chnerch A., Schhein J.B., Jones S.J. M., Marra M.A.,

Human and mouse cpNA sequences.",

Ill Mannan and mouse cpNA sequences.",

Ill Mannan and mouse cpNA sequences.",

Ill Fallow D. Netton B. Well S. Sci. U.S.A., 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                "Prediction of the coding sequences of unidentified human genes. IX The complete sequences of 100 new cDNA clones from brain which can
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Kalicki J., Elliott G.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May act as a scaffolding protein involved in the
corganization of synaptic active zones and in synaptic vesicle
trafficking (By similarity).
-!- SUBUNIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 similarity).
-!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        IsoId=Q9Y6V0-2; Sequence=VSP 003923, VSP 003924, VSP 003925
VSP 003926, VSP 003927;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Note=No experimental confirmation available;
-!- DCMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                        Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                      SEQUENCE OF 552-4404 FROM N.A.
Kraemer J., Wollam C., Wohldmann P., McGrane B.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing, Named isoforms=2, Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                  SEQUENCE OF 3619-5147 FROM N.A. (ISOFORM 2)
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DNA Res. 5:31-39(1998).
                                                                                                                                                                                                                                                                   MEDLINE=98290545; PubMed=9628581;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 4405-4439 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE OF 4405-5147 FROM N.A.
                                                                                                                                                                                                                                      TISSUE=Brain;
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Name=2 Name=1

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QTGKLMEG (in isoform 2).
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P-A-K-P-G-P-Q-Y-X.
C4-TYPE (POTENTIAL).
C4-TYPE (POTENTIAL).
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GO: GO:0005826; C:cytoskeleton; NAS.

GO: GO:0005502; C:synaptic junction; ISS.

GO: GO:0005509; F:calcium ion binding; ISS.

GO: GO:0005522; F:calcium-dependent phospholipid binding; ISS.

GO: GO:0005522; F:calcium-dependent phospholipid binding; ISS.

GO: GO:0005522; F:calcium-dependent phospholipid binding; ISS.

GO: GO:0005522; F:calcium-dependent phospholipid binding; ISS.

GO: GO:0005522; F:calcium-dependent phospholipid binding; ISS.

RO: GO:0005522; F:calcium-dependent phospholipid-binding; Zinc; Metal-binding; Zinc-finger;

RR PROSITE; PSO0049; C2-DOMAIN 1; 1.

RR PROSITE; PSO0049; C2-DOMAIN 2; 2.

Calcium/phospholipid-binding; Zinc; Metal-binding; Zinc-finger;

NON_TER
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4576 4576 G-AGVWTVQRAS (in isoform 2).

4757 4761 TAHKS -> SKRRK (in isoform 2).

4757 4761 TAHKS -> SKRRK (in isoform 2).

4762 5147 Missing (in isoform 2).

4762 5147 Missing (in isoform 2).

5147 AA; 563537 MM; CD5D84990498CD3C CRC64;
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/FIId=VSP_003923.
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C2 DOMAIN 2.
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EMBL; AC004903; AAD20936.1; --
EMBL; AC004886; AAD21789.1; --
EMBL; AC004886; BAAD21789.1; --
EMBL; BC001304; AAH01304.1; --
EMBL; AC004082; AAB97937.1; --
EMBL; AC064082; AAB97937.1; --
EMBL; AC0634; T00634.
HSSP; P04410; 1A25.
Genew; HGNC:13406; PCLO.
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1449 DFIRKQIIEMSADEDASGSEDDEFIRNQLKEISSSTESQKKEETKGKGKITAGKHRR--- 1505 2555 SSSLPRVSTWRRTGSSSSILSASS---ESSEKAKSEDEKHVNSISGTKQSKENQVSAKGT 2611 1338 PEQPKDQEKTQSLSETLEITISEEEIKESQEERKDTFKKDSQQDIPSSKDHKEKSEFVDD 1397 2017 IPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRL-KGDNEKHSPRNMGGILGED 2075 2182 ESESKGIK--GGKKVYKSLITGKVRSNSEI-----SGGMKQPL-----QANMPSIS- 2225 -----RGRTMIH----IPGVRNSS-----SSTSPVSKKGPPLKTPASKSPSEG-- 2264 1602 SPEDRSRGEGSSSLHASSFTPGTSPTSVSSLDEDSDSDSSPSHKKGESKQQRKARHRPHGPL 1661 1158 SAPEEQKHDLLKSQVQIAEEKLEGRVAPKTVQEGKQPQTXMEGLPSGTPQSLPKTDDKTT 1217 2377 NLTK-OTGLS----KNASSIPRSESASKGL------NOMNNGN-----GANKKVEL------RPVLVROSTKS---SGSESDRSE-----RPVLVROSTFIKE 1837 EKEPLYGGMLIEDYIYESLVEDTYNGSVDGSLLTRQEEENGFWQQKGREQKIRLSEQIYE 2447 APS---PILRRKLEESASFESLSPSSRPASPIRSQAQIPVLSPS--LPDMSLSTHSSVQA 2265 -QTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQS GGW------RKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKH : | : | | | : | | | : | | | : | | | : | | | | : | | | | : | | | | : | | | | : | | | : | | | : | | | : | | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : -----PQASGYAPKSFHVED 2651 VSKTEDVWVRIEDCP------INNPRSGRSPTGNTPP---1911 QAJAKQPINRGQPKPILQKQ------STFPQSSKDIPDRGAA--2502 2226 2417

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IN REF
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EMBL; U30872; AAA82935.1; -.
EMBL; U25725; AAA8689.1; -.
PIR; PC4035; PC4035.
Genew; HGNC:1857; CENPF.
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-1- FUNCTION: Probably required for kinetochore function, involved in chromosome segregation during mitosis. Interacts with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhu X., Chang K.-H., He D., Mancini M.A., Brinkley W.R., Lee W.-H.;
"The C terminus of mitosin is essential for its nuclear localization,
centromere/kinetochore targeting, and dimerization.";
J. Biol. Chem. 270:19545-19550(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=55379648; PubMed=7651420; Zhu X., Chen C.-F., Shan B., Zhu X., Mancini M.A., Chang K.-H., Liu C.-Y., Chen C.-F., Shan B., Cones D., Yang-Feng T.L., Lee W.-H.; "Characterization of a novel 350-kilodalton nuclear phosphoprotein that is specifically involved in mitotic-phase progression."; Mol. Cell. Biol. 15:5017-5029(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2194-3210 FROM N.A.
MEDLINE=95336446, PubMed=7612011;
Li Q., Ke Y., Kapp J.A., Fertig N., Medsger T.A. Jr., Joshi H.C.;
Li A novel cell-cycle-dependent 350-kDa nuclear protein: C-terminal
domain sufficient for nuclear localization.";
Biochem. Biophys. Res. Commun. 212:220-228(1995).
                                                                                                                                                                                                                                                                     Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM.N.A.

TISSTB=Breast carcinoma;

MEDLINE=95348175; PubMed=7542657;

Liao H., Winkfein R.J., Mack G., Rattner J.B., Yen T.J.;

"CENP-F is a protein of the nuclear matrix that assembles onto kinetochores at late G2 and is rapidly degraded after mitosis.";

J. Cell Biol. 130:507-518(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE=98437347; PubMed=9763420; Chan G.K.T., Schaar B.T., Yen T.J.; "Characterization of the kinetochore binding domain of CENP-E reinteractions with the kinetochore proteins CENP-F and hBUBRL."; J. Cell Biol. 143:49-63(1998).
                                                                                                                                                       CENF HUMAN STANDARD, PRT; 3210 AA.
P49454; Q13171; Q13246;
01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
CENP-F kinetochore protein (Centromere protein F) (Mitosin)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=20459117; PubMed=10852915;
Ashar H.R., James L., Gray K., Carr D., Black S., Armstrong Bishop W.R., Kirschmeier P.;
"Farnesyl transferase inhibitors block the farnesylation of and CENP-F and alter the association of CENP-E with the
2165 ASSIIESVVPKPEGPVADTVSTDLLISEKDPVKKAKKETGNGII--
                                                                      2773 -PSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTP 2808
                                                                                     MEDLINE=95370296; PubMed=7642639;
                                                                                                                                                                                                                                                         Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                             NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         microtubules.";
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the FNBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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T -> A (IN REF. 2).

G -> D (IN REF. 2).

MISSING (IN REF. 2).

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V -> A (IN REF. 2).

V -> L (IN REF. 2).

ER -> DG (IN REF. 2).

ER -> DG (IN REF. 3).

D -> N (IN REF. 3).

D -> N (IN REF. 3).

EX -> Q (IN REF. 3).

D -> N (IN REF. 2).

ELNERVAALHNDQBACK -> SSWREWQPCIMTKKPVS
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retinoblastoma protein (RB), CENP-E and BUBR1.
SUBUNIT: Homo- or heterodimer.
SUBCELLULAR LOCATION: Nuclear matrix (but not in the nucleolus),
reorganization to the Kinetochore/centromere (coronal surface of
the outer plate) and the spindle during mitosis.
DEVELOPMENTAL STAGE: Gradually accumulates during the cell cycle.
PTM: Hyperphosphorylated during mitosis.
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MIM; 600236; -...
MIM; 600256; -...
GC; GC:0005634; C:Nucleus; TAS.
GC; GC:0005639; C:Spindle; TAS.
GC; GC:0005819; C:Spindle; TAS.
GC; GC:000067; P:DN replication and chromosome cycle; TAS.
GC; GC:0007067; P:DN replication of mitosis; TAS.
GC; GC:0007068; P:regulation of mitosis; TAS.
Chromosomal protein; Nuclear protein; Centromere; Coiled coil;
Mitosis; Phosphorylation; Antigen; Cell cycle; Repeat; Polymorphism;
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NUCLEAR LOCALIZATION SIGNAL (POTENTIAL)
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K -> N (in dbSNP:7289)
/FTId=VAR 014839.
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2.6$; Score 385.5; DB 1;
Local Similarity 17.9$; Pred. No. 6.6e-07;
les 577; Conservative 502; Mismatches 1239;
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1411 FLSLQSEHKILHDQHCQMSSRMSELQTYVDSLKAENLVLSTNLRNFQGDLVKEMQLGLEE 1470
1243PQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSAEDEIGCNQTTQ 1294
1295 EADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRL 1337 :
1338 QGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSP 1372
1373 PEHYVQETPLMFSRCISVSSL-DSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGGTM 1431 1642 AKGVEELESLCEVYRQSLEKLBEKMSSQGIMKNKEIQELEQLLSSERQEL 1691
1432 PPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDAD 1486
1487 TLLHFATESTPDGFSCSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPK-ES 1545
1546 NENQEKEAEKTIDSEKDLLDDSDDDIBILEECIISAMP-TKSSRKGKKPAQTASKLPPP 1604 1:
1605 VA-RKPSQLPVYKLLPSQNRLQP-QKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTI 1662 :
1663 ESPPNELF 1684 : 1894 ESLLNEMKELDSKLHLQEVQLMTKIEACIELEKIVGELKKENSDLSEKLEYFSCDHQELL 1953
1685 EKRDTIPTEGRSTD-BAQGGKISSVIIPELDDNKAEEGDILAECINSAMPKGKS 1737 :::
1738HKPFRVKKIMDQVQQASASSSAPNKNQLDGKKKK 1771
1772 PTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDSKKQNLKNNSKDFNDKLPNNE 1831 2069 KITALDQLSEKNKEKTQELESHQSE-CLHCIQVAEAEVKEKTELLQTLSSDVSELLK 2124
1832 DRVRGSFAFDSPHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESE 1891
1892 AKVTSHTELTSNQOSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRG 1944
1945AATDEKLONFAIENTPVCFSHNSSL-SSLSDIDQE-NNNKENEPIKETEPPDS 1995 AATDEKLONFAIENTPVCFSHNSSL-SSLSDIDQE-NNNKENEPIKETEPPDS 1995
1996 QGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPK 2049
2050 KKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGAN 2109 :
2110 SIVSSLHQAAAAACLSRQASSDSDSILSLKSGI-SLGSPFHLFPD 2153

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2387 PPIESEHQLRNSIEKLRARLEADEKKQLCVLQQLKESEHHADLLKGRVENLERELEIART 2446
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                     QEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQM
                                                                 2214 KQPLQANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRG
                                                                                                                                                         2334 NGISPPNKLSQLPRISSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPR
                                  2274 AKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGR
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                                                                                       2494 TNELOKEOERISELE-----IINSSFENILQEKEQEKVOMKEKSST------
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MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MEDLINE=97405699; PubMed=9260743;
MAD., Northias F., Boyne L.J., Fischer I.;
Mad., Northias F., Boyne L.J., Fischer I.;
In rat CNS and PNS during development.";
In rat CNS and PNS during development.";
In rat CNS and PNS during development.";
In rat CNS and PNS during development.";
PNORTION: The function of brain MAPS is essentially unknown.
Phosphorylated MAPIB may play a role in the cytoskeletal changes
that accompany neurite extension. Possibly MAPIB Binds to at least
two tubulin subunits in the polymer, and this bridging of subunits
might be involved in nucleating microtubule polymerization and in
stabilizing microtubules.

--- SUBUNIT: 3 different light chains, LCI, LC2 and LC3, can associate
with MAPIA and MAPIB proteins.

--- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
booth or many cerebrum). Not expressed in liver, spleen, kidney,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the ENBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/amnounce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       postnatal development and are low in adults. In derease during postnatal development and are low in adults. In derease during ganglia levels remain high throughout development. In dorsal root ganglia levels remain high throughout development.

INDUCTION: By nerve growth factor.

INDUCTION: By nerve growth factor.

INDUCTION: By nerve growth factor.

KKEE and KKIZI/V. repeated but not at fixed intervals, which is responsible for the binding of MAPIB to microtubules.

PTM: LCI is coexpressed with MAPIB. It is a polypeptide generated from MAPIB by proteclytic processing. It is free to associate with both MAPIB, and MAPIB. It interacts with the amino-terminal region of MAPIB. (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cortex, spinal cord and sciatic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Spinal cord;
MEDILINE-90059811, PubMed=2555150,
Rienitz A., Grenningloh G., Hermans-Borgmeyer I., Kirsch J.,
Littauer U.Z., Prior P. V., Gundelfinger B.D., Schnitt B., Betz H.;
"Neuraxin, a novel putative structural protein of the rat central nervous system that is immunologically related to microtubule-associated protein 5.";
EMBO J. 8:2879-2888(1989).
                                                                                                                                                                                              Liu D., Fischer I.; "Isolation and sequencing of the 5' end of the rat microtubule-associated protein (MAPIB)-encoding cDNA."; Gene 172:307-308(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zauner W., Kratz J., Staunton J., Feick P., Wiche G.; "Identification of two distinct microtubule binding domains recombinant rat MAP 18.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY
                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION. STRAIN-Sprague-Dawley; TISSUE-Brain, and Glial tumor; MEDLINE-92347374; PubMed=1639092;
[1]
SEQUENCE OF 1-142 FROM N.A.
STRAIN=Sprague-Dawley, TISSUE=Testis;
MEDLINE=96257242; PubMed=8666295;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     heart or muscle.
DEVELOPMENTAL STAGE: In cerebral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eur. J. Cell Biol. 57:66-74(1992)
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CAUTION: A C-terminal
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EMBL; X60370; CAC16162.1; -. EMBL; X16623; CAA34620.1; ALT_SEQ. PIR; AS6577; AS6577.

EMBL; US2950; AAB17068.1; -.

MAPB RAT STANDARD; PRI; 2459 AA.
P15205; 062958; Q9ER21; Q9QW92;
01-APR-1990 (Rel. 14, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1

MAPB

Eukaryota; Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

Rattus norvegicus (Rat). light chain LC1]. MAPIB.

NCBI TaxID=10116;

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K------TIQAHDVGGYYYEKTERTIKSPCDSGYSYBTIEKTTKTPEDGGYSCEITEK 1936
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| SSSSPPI-----DAAAEFYGFRS
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                                                      CFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQ-GEPSKPQASGYAPKSFHVEDTPVC
                                                                                                          FSRNSSLSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGD-----NEKHSPRNMGGILG
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 -- KDIPDRGAATDEKLQN---FAIENTPV
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T -> S (IN REF. 1).
R -> K (IN REF. 3).
L -> I (IN REF. 3).
W, 2E3F6872DEDB8BA2 CRC64;
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                                                                                                                                                            Event-Alternative splicing, Named isoforms=1;
Comment=A number of isoforms are produced;
Name=1; Synonyms=480-kDa isoform;
Isocd=2012955-1; Sequence=Displayed;
-! TISSUB SPECIFICITY: Expressed in brain and other tissues. Isoform
-! SIMILARITY: Contains 23 ANK repeats.
-! SIMILARITY: Contains 1 death domain.
                                                                                                               Bukaryota, Merazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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R HSS; PS575; A55575.
R HSSP; PS5273; 1B18.
R Genew; HGNC1494, ANK3.
R GATE, CO16665; P: Protein targeting; NAS.
R INTERPOOL IPRO0048; Death.
R INTERPOOL IPRO0048; Death.
R Fram; PRO0021; ank, 24.
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R PROSIT; PRO019; ZUS; I.
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R REPEAT 204 205 ANK 6.
R REPEAT 205 ANK 7.
                                          28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-MAR-2004 (Rel. 43, Last annotation update)
Ankyrin 3 (ANK-3) (Ankyrin G).
                     PRT; 4377 AA.
                    STANDARD;
                                                                                                       Homo sapiens (Human)
                   ANK3 HUMAN
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	4377; 1051; Gaps 147;	.VKLRSKMS 92 : : ATLQEKISSATNSV 1752	SSRSGEC 110	YAQLQNLTKR 168	::: ALLSPIKTLTTE 1862	RIARIQQIEKDI 228 : :::: : DVAEMKEDL 1912	INMATSGNG 277 :: ILKKDVCVDNKG 1972	SLLS 3	: PERVQVKAKAASEKDYNLTK 2032	KDSVLLGNSRGS 376 : MPPASMRTSTSE 2092	OEAHEPGMDQDK 435 	AMNELGGL 47	 /H 2171	ANKAT 518	PAPT 22	35 VARLMECALE 5 / 8	TLAIIESGGGI 638	: TTRMVYHSPPG- 2259	
15768B684 CRC64;	; DB 1; Length .4e-06; es 1178; Indels	DLLERLKELNLDSSNFPGVKL -:	GSREGSV	SLLĻADLDKE	: : : : : : : : : :	MEEQLGTCQDMEKRAQRRIARIOQIEKD : : : : TPSSLSSSQEILKDVAEMKED	SSQNKHETGSHDAERQNEGGGVGEINMATSGNG 	SS -	AAASQSPSLPERVQVKA	RTLLAMSSSQDSCISMRQSGCLPLIQLHGNDKDSVLLGNSRG : :	IHSQPDDXRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGMDQDX 	CPAVCVLMKLS	:: :: HEV-PIPPVITETRTEVVH		VIRSIUFSAGUVFGIQFEBFVSFRFSFIFRED	LCSTRECUCALVAQUAS SEBELLOGO ATAS VLRN LSWRALVNSKAL LKEVGSVAALMYE 	VKKESTLKSVLSALMNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIE	, <u>T</u>	LRNVSSLIATNEDHRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNP : : : : : : : : :
ANK 9. ANK 10. ANK 11. ANK 11. ANK 13. ANK 14. ANK 14. ANK 16. ANK 17. ANK 17. ANK 17. ANK 20. ANK 20. ANK 20. ANK 20. ANK 21. ANK 21. ANK 22. ANK 23. SER-RICH. 399 MW; F42379E5	.6%; Score 380.5 .3%; Pred. No. 1 e 430; Mismatch	SIEDEAMASSGQI : HAEVALVNGSI	LRSY	VNGSRESTGYLEEL	VVNVLPEPALKK	SLQTDLTRRQLEYEARQIRVAME : : :::: SRTSSPVKSSLFLAPSALKLSTP	OSQATEAERSSQNKHETGSHDAER	HETASVLSS	PKSPKSDKGHSPEDDWIEFSSEEIREARQQAAASQSPSL	MLGTHDKDDMSRTLLAMSSSQDSCISMRQSG ::	IHSQPDDKRGRREIRV	PAPVE	: PLSDSGFETRSEKTPSAPQSAETTGPKPLFHEV	SI	TITLE TO THE TOTAL	LCSMRGCRRALVAGLASESEDIGQVIASVLA : :: : : : : : TSSIKEKVKAFQMKASSEEDDHNRVLSKGMR	NLSAHCTENKADICAVI	 HIT	DILRENNCLQTLLQHLE:
333 366 396 432 432 4428 443 461 465 498 531 531 537 630 630 640 653 663 663 663 725 725 729 725 729 745 748 748 748 748 748 748 748 748 748 748	2. Similarity 18. 5; Conservative	TEASNMKEVLKQLQG :: : : TMASSLSSPVKQMPG	SAVVERVERVER	PVPMGSFPRRG	SSVTSSIITVPVYSV	IDSLPLTENFSLQTDL : : THPQPHFSRTSSP	LRIRQLLQSQATEAER : : : : MRMTAILOTDVPEEKP	OGSTTRMD	S PKS PKS DKGHS PED	MLGTHDXDDMSRTLL ::	KEARARASAAL-HNII 	WdN	: : SPLSDSGFETRSEKT			:- - :- :- SIKEKVKAFQMKA	VKKESTLKSVLSALW	: : VKEET	JRNVSSLIATNEDHR(
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1668 3175	PELD 171-
1715	DNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNK- 1762
1763 3279	NQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAER 1803
1804	VFSDNKDSKKQNLKNNSKDFNDKLFNNEDRVRGSFAFDSPHHYTPIEG 1851 : : :
1852	TPYCFSRNDSLSSLDFDDDVDLSREKAELR-KAKENKESEAKVTSHTEL 1900
1901	TSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQSSKDIFDRGAATDEKLQNFAIEN 1958
1959	RHPDRSVFPDTYFSYKVDEEFATPFXTVATKGLPFDFWSNNRGDBEVFDSKSREDE 3563
1990	TEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSID 2033
2034	-SEDDLLOECISSAMPKKKRPSRLKGDNEKHSPRNMGGILGEDLTLDLKD 2082
2083	IQRPDSEHGLS-PDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSG 2141 ::
3726	ISLGSPFHLTPDQEEKPFTSNKG
2174	NENNNNLDSSTIQTDNIMSNIVLTEHSAPTCTTEKDNPVKVSSGKKTGVLQGHCVRD 3842
3843	NSEISGOMKOPLOANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPAS 2258
2259 3888	KSPSEGQTATTSPRGAKPSVKSELSPVA KMKQVSQSEKTKAL
3926	RPIGSPGRNSISPGRNGISPPNKLSQLP
2366	YTSPGROMSQQNLTKQTGLS-KNASSIPR-SESASKGINOMNNGNGANKKVELSR 2418
2419	MSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLBESASFESLSPSSRPASP-TRS 2477 :
2478	QAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPS 2537

4339 PRLSLHBEEGSSGS 4352	Db 433	
2824 ESSGTQSPKRHSGS 2837	Qy 282	
4293 VEEPASPLAAYQKSLBETSKLIIBETKPCVPVSMKKMSRTSPADGK 4338	Db 429	
ARVTPENYNPSP	Qy 277	
4HTEITPEAKTKSYPPESQNDVGKQSTKETLKPKIHGSGH 4292	Db 4254	
2712 PMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPFSSSSSK 2769	Qy 271	
8NLESCAQARRVTGGLLDRLDDSPDQCRDSITSYLKGEAGKFEANGS- 4253	Db 4208	
2652 SKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSV 2711	Qy 265	
4178 GNISGTRSFADENNVFHDPVDGWQNETSSG	Db 417	
2593 NSISGTKO-SKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAESKTLIYQMAPAV 2651	Qy 259	
9 SL-ISQSFMLLKKRWTRDGKNATTDALTSVLTKINRIDIVTLLEGBIFDY 4177	Db 4129	
2538 RLPINRSGIWKREHSKHSSSLPRVSIWRRIGSSSSILSASSESSEKAKSEDE-KHV 2592	Qy 253	

Search completed: August 25, 2004, 17:16:32 Job time : 76.5 secs

Scoring table:

Searched:

Minimum DB 8 Maximum DB 8

Database

Perfect score:

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Run

Sequence:

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Q8vq99 staphylococ
Q9v736 drosophila
Q8uq35 draphylococ
Q9uq35 homo sapien
Q9qq4 staphylococ
Q8liff caenorhabdi
Q2127 caenorhabdi
Q7230 caenorhabdi
Q7238 ashbya goss
Q8iff caenorhabdi
Q7xxnl oryza sativ
Q9xxl oryza sativ
Q9xxl drosophila
Q9vh10 drosophila
Q9vrg8 drosophila
Q9vrg8 drosophila
Q8vrg8 drosophila
Q8vrg8 streptococc
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076891 drosophila
08cmu7 staphylococ
09haw6 homo sapien
09vc00 drosophila
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29vtn2 drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-1997 (TrEMBirel. 02, Created)
01-MAY-1997 (TrEMBirel. 03, Last sequence update)
01-OCT-2003 (TrEMBirel. 25, Last annotation update)
Adenomatous polyposis coli.
Xenopus laevis (African clawed frog).
Xenopus laevis (African Clawed frog).
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
11-InxID-8355;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 13; Length 2829;
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Vleminckx K., Wong B., Guger K., Gumbiner B.M.;
Vleminckx (UUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64442; AAB41671.1;
INTERPRO; IPR008938; ARM.
INTERPRO; IPR00225; Armadillo.
Pfam; PF00514; Armadillo.seg; 4.
SPMRT; SM00185; ARM; 5.
SEQUENCE 2829 AA; 310878 MW; 8A2BABDB7706E496 CRC64;
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Pest Local Similarity 74.3%; Pred. No. 0;
Matches 2128; Conservative 263; Mismatches 416; Indels
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                                                                                                                 August 25, 2004, 17:05:26; Search time 183.5 Seconds (without alignments) 4888.383 Million cell updates/sec
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                                                                                                                                                                                                                          1 MAAASYDQLLKQVEALKMEN......ESSGTQSPKRHSGSYLVTSV
                   GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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                                                                                                                                                                                                                                                                                                             1017041 seqs, 315518202 residues
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121 RGFVNGSRESTGYLBELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180

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STRAIN=C57BL/G1 TISSUE=Adipose tissue;

MEDLINE=22394683; PubMed=12466851;

The FINTOM Consortium,

The FANTOM Consortium,

The RIKEN Genome Exploration Research Group Phase I & II Team;

The Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

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Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";

EMBL; AKO80907; BC08073.1; -.

MGD; MGI:88039; Apc.

GO; G0:0008034; C:nucleus; IDA.

RG); G0:0008034; C:nucleus; IDA.

RG); G0:0008034; C:nucleus; IDA.

RG); G0:0009959; P:anterior/posterior pattern formation; IMP.

RG); G0:0009959; P:anterior/posterior pattern formation; IMP.

RG); G0:0009059; P:anterior/posterior pattern formation; IMP.

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TGLS KNASS I PRSESASKGLNOMNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQS
                                                                                                                                               SGLPKTHSSIPRSESASKSINQ-NVNTGSNKKVELSRMSSTKSSGSESDRSERPALVRQS
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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(Fragment).
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540 538 009 598 660 658 720 718 780 840 900 2 420 480 478 360 358 418 118 180 240 238 300 298 120 178 09 9 CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDMGAVSMLKNLIHSKHKMIAM NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE HGNDKDSVLLGNSRGSKEARARASAALHNI IHSQPDDKRGRREIRVLHLLEQIRAYCETC VDCEMYGLTNDHYSVTLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL QOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLISFDEEHRHAMNELGGLQAIAELLQ WEWQEAHEQGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSWLKNLIHSKHKMIAM GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKOKALEAELDAQHLSETFDNIDNLS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGS LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC 1 MAAASYDQLLKQVBALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDETM 61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 61 -TSGQIDLLERLKEFNLD-SNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 121 RGFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPITENFSL 181 QTDLTRRQLEYBARQIRVAMBEQLGTCQDMEKRAQRRIARIQQIBKDILRIRQLLQSQAT EAERSSONWHETGSHDAERONEGOGVGEINMATSGNGOGSTTRMDHETASVLSSSSTHSA 1 MAAASYDOLLKQVEALKMENSNIRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM Gaps 7 Length 1056; Indels 35.4%; Score 5156; DB 11; 94.9%; Pred. No. 3.2e-246; iive 23; Mismatches 29; Query Match
Best Local Similarity 94.9
Matches 1004; Conservative 599 841 119 479 901 899 196 179 239 299 361 421 419 479 541 539 601 661 629 721 719 781 959 241 301 359 481 셤 9 & 9 19 & 9 8 a 8 g & 셤 ò ద Ś ò ઠે g ò 쉽 ò g 8 ò g ద ò g ò

LDTPINYSLKYSDEQLNSGROSPSONERWARPKHIED 105	QY 1.8SSSTHSAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISWRQSG 351
1019 LDTPINYSLKYSDEQINSGRQSPSQNBRWARPKHVIED 1056	270SKVEVVFWLLSWLATRDQEDTARTLLAMSSSPESCVAMRRSG
RESULT 3 Q921K7 ID Q921K7 PRELIMINARY; PRT; 2274 AA.	Qy 352 CLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLH 408
01-MAY-1999 (TrEMBLrel. 10, Created) 01-MAY-1999 (TrEMBLrel. 10, Last sequence update) 01-CCT-2003 (TrEMBLrel. 25, Last annotation update)	QY 409 LLEQIRAYCETCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHANNE 468
procein. musculus (Mouse). Tyota: Metazoa; Chordata; Craniata; Vertebrata; E	QY 469 LGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLFFGDVANKATLCSMKGCMRA 528
ae;	CY 529 LVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSV 588
s=99147086; J.H., Kirk A., Kuipers ification o	Cy 589 LSALWNLSAHCTENKADICAVDGALAFLYGTLTYRSQTNTLAIIESGGGILRNYSSLIAT 648
: suppressor."; Bol. 9:105-108(1999). AJ130793: CAAJ0207.1; AJ130784; CAAJ0207.1; JOINED.	649 NEDHROLLRENNCLOTLLOHLKSHSLTIVSNACGTLWNLSARNPKDOEALWDMGAVSMLK : : :
AJ130789; AJ130790; AJ130791; AJ130792;	QY 768 HLSETFDNIDNLS-PKASHRSKQRHKQSLYGDTVFDTNRHDDNRSDNFNTGNMT- 820
AJ130794; CAA10207.1; AJ130794; CAA10207.1; AJ130795; CAA10207.1; AJ130796; CAA10207.1;	QY 821VLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSS 874
1346052; Apc 1346052; Apc 118008938; 118000225;	Qy 875 KRGLQISTTAAQIAKVMEEVSAHITSQEDRSGGSTTELHCVTDERNALRRSSAAHTHSNT 934 ::
Pantne_S. illo_seg; 3. oSPHOPANTETHEINE; 1.	QY 935 YNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKPSIESYSEDDES 992 :
24.1%; Score 3508.5; DB 11; Length 2274; Similarity 34.4%; Pred. No. 2e-164.	QY 993 KFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWARP 1052 DD 937CPLAALAEHRDD
CONSCIVACIONE 300; HISMACINES 709; INCELS YYDQLEKQVEALKOVENENSNLRQELEDNSNHLTKLETEASNMKEVLKQLC 1	QY 1053 KHIIEDEIKQSEQRQSTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSET 1112
SSGQIDLLERLKEINLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPRR	QY 1113 NRVGSNHGINQNVSQSLCQEDDYEDDKFTNYSERYSEBEQHEBEBERPTNYSIKYNEEKRH 1172 Db 1003GVRPLVGPGTS
-GFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLONLTKR.LDSLPLTENFSL 	Qy 1173 VDQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLH 1232
QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQ	QY 1233 PSSAQERSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQT 1292
	QY 1293 TOBADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLS 1343

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1344 SESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIAS 1403 	1404 SVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPKNKA 1457 	1458 PTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEPF1Q 1517	1518 KDVELRIMPPV-QENDNGNETESEQPKESNENGEKEAEKTIDSEKDLLDDSDDDDIE 1573 	ILEBCIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFT 16	1328 ALRECLGAAMPARLERKVASALVPGRKSLFVFVYMLVFAFAK 1368 1634 PGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAGGEFEKRDTIPTE 1693	-GDD-SGTDSAEGTPVNFSSAASLSDETLQGPSRDKPAGPGDRQKPT-	1694 GRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQA 1753 : : : : 414 GRAAAROKAA 1430	SASSSAPNKNQLDGKKKKPTSPVKPIPQNTEY-RTRVRKNADSKNNLNAERVFSDNKDSK		KONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDV	1467 CQTYDSDEE 1499	1873 DLSREKAELRKAKENKESEAKVISHTELISNQQSANKTQAIAKQPINRGQP 1923	KPILOKOSTFPOSSKDI PDRGAATDEKLONFAIENTPVCFSHNSSLSDI DOENNNKE 19	:	SEPSKPQASGYAPKSFHV	1567SPRANDARGPEQGSKQDSSPSPRAEBELLQRC1 1603	2044 SSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIORPDSE-HGLS 2093 :: :	PDSENFDWKAIOEGANSIVSSLHOAAAAACLSRQASSDSDSILSLKSGISLGSPFHLT 215	:: : :	2152 PDQEEXPPTSNKGPRILKPGEKSTLETKKI-ESESKGIKGGKKVYKSLITGKVR-SNSEI 2209	1703PSKLRKGRKPAAEAGGAWRPEKRGTTSTKINGSPRLPNGPE 1743	2210 SGQMKQPLQANMPSISRGRIMHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSBGQTAIT 2269	1744 KAKGIQKAMAGESIMLRGRIVIYSAGPASRIQSKGISGPCTIPKKTGISGTT 1795	SPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSI 		2330 SPGRNGISPPNKLSQLPRISSPSTASIKSSGSGKMSYTSPGRQMSQQNLIK 2380 1835 PPARLAKTPSSSSSQTSPASQPLPRRSPLATPIGGPLPGPGGSLVPKSPARALLAK 1890	н
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2541 INRSGTWKREHSKHSSSLPRVSTWRRTGSSSSLLSASSESSEKAKSEDEKHVNSIS--GT

1891 QHXTQKSPVRIPFMQRPARRVPPPLARPSPEPGSRGRAGAEGTPGARGSRLGLVRWASAR 1950

1951 SSGSES--SDRSGFRRQLIFIKESFG-LLRRRRSELSSADSTASTSQAASPRRGRPALPA

2424 SSGSESDRSERPVLVROSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPV

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2484 L---SPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLP

2190 SGPVAPQGSD------VLTKPPASAPFP--HEGLSAVIAGFP-----TSR 2230

HSSPSGTVAARVTPFNYNPSPRKSS--ADSTSARPSQIPTPVN 2810 2231 HGSPSR--AARVPPFNYVPSPMAAATWASDSAVEKAPVSSPAS 2271

2770

2710 SVPMRTVGLENRLISFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERTPFSSSSSK 2769 2154 RKTSDAVVQTEDVATSKTNSSTSPSLESRDPP-----A

2652 SKTEDVWYRIEDCPINNPRSGRSPT--GNTPPVIDSVSEKANPNIKDSKDNGAKONVGNG 2709

2115

2599 KOSKENOVSAKGTWRKIKENEFS-----PTNSTSQTVSSGATNGAESKTLIYQMAPAV

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases Koyama K., Nakagawa H., Nakamura Y.; "APCL exon14."; PRELIMINARY; SEQUENCE FROM N.A. SEQUENCE FROM N.A. 095996; 4, RESULT 966560 HE STATE OF THE ST

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DR GO; GO:0008013; F:beta-catenin binding; TAS.	Db 799 PAALSLFLGSPFLOGOALA	PAALSLFLGSPFLOGGALARTPPTRRGGKEAEKDTSGEAAVA 840
DR GO; GO:0006461; P:protein complex assembly; TAS. DR GO; GO:0007165; P:signal transduction; TAS.	OV 874 SKRGLOISTTAAOIAKVME	CVTDERNALRRSSAA
DR InterPro, IPR008938, ARM. DR InterPro, IPR000225, Armadillo.	841	GDPGQEAPREGRAQSCSP
DR InterPro; IPR01818; Pept_MIOA_M12B. DR Pfam; PF00514; Armadillo_Seg; 3.	QY 933 -NTYNFTKSENSNRTCSMP	-NTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKPSIESYSEDDE 991
DR SMAKI; SMULES; ARM; 5. DR PROSITE; PS00546; CYSTENE SWITCH; 1.	Db 895 CRGPEGGRREAGSRAHPLLI	CRGPEGGRREAGSRAHPLLRLKAAHASLSNDSLNSGSASDGYCPREHM 942
Diery Match 2303 ms; 215340 ms; 7559401603ACD615D C	Qy 992 SKFCSYGQYPADLAHKIHS	SKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWAR 1051
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64 LVSSGQTEVLEQLKALOMDITSLYNLKROPPAARTPEGSPV-HGSGP	Db 967	LDLDLPGCQAEPPAREATSADARVRTIKLSPTYQ 1000
KEBKEKDWYYAQLQNLTKRIDSLPLTE-N	Qy 1172 HVDQPIDYSLKYATDIPSS(HVDQPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQL 1231
Db 116 SKDSFGELSRATIRLLEELDRERGFLLNSIEKEEKEKLMYYSQLQGLSKRLDELPHVETQ 175	1 000	
178 FSLQTDLTRRQLEYEARQIRVAMEEQLGTCQDMEXRAQRRIARIQQIEKDILRIRQLLQS	1032	
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238 QATEAERSSQNKHETGSHDAERQNEGGGGGGEINMATSGNGGGSTTRMDHETASVLSSSST	Db 1087 GGDLDDSDSSLEGLEE	GGDLDDSDSSLBGLEEAGPSBAELDSTWRAPGATSLPVAIPAPRRNRGRGLGV 1139
DD ZZSAQDRVQQ!EFQALLAV	Qy 1345 ESARHKAVEFPSGAKSPSK	ESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASS 1404
263 DGTPQPGNSKVEVVFWLLSMLATRDQBDTARTLLAMSSSPESCVAMRRSGGLPLLL	Db 1140 EDA	TPSSSSENYVQETPLVLSRCSSVSSLGSFESPSIASS 1179
QY 358 QLLHGNDXDSVLLGNSRGSKEARARASAALHNIH9QPDDKRGREBIRVLHLLEQIR 414	Qy 1405 VQSEPCSGMVSGIISPSDLI 	VQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTREVPKWKAPTAEK 1462 The processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processory of the processor
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QY 415 AYCETCWEWQEAHEPGMD-QDKNPMPAFVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQ 473	1233	
4 AIABLLQUDCEMYGLTNDHYSITLRRYAGNALTHITHTHEGDVANKATLCSWKGCWRALVAGL	1520	
Db 439 AVAELLQVDYEMHKATRDPLNLALRRYAGMTLTNLTFGDVANKATLCARRGCMEAIVAQL 498	1292	
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OY 654 QILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHS 713	Qy 1700 AQGGKTSSVTIPELDDNKAI 	AQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSA 1759
DD 619 QVLRDHNCLGTLLQHLTSHSLTIVSNACGTLWNLSARSARDQELLWDLGAVGMLRNLVHS 678	1760 PNKNQLDGKK	NADSKNNLNAERVFSDNKD
QY 714 KHKMIAMGSAAALRNIMANRPAKYK-DANIMSPGSSLPSLHVRKQKALEAELDAQHLSET 772	::: 1452 AEQSRGAGKNRAGLELPL	: : DKD
0.75 KAIN'I ANGOARALINNILANGKAANIQAAA IAYSEGOCYESI KYKQKALISAEDIA 1773 EDNITINNI GOKBEHD CKO	Qy 1811 SKKQNLKNNSKDFNDKLPNN	SKKONLKONSKDENDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDD 1870
739 LEHLEKOGPPAAEAATKKPLPPLRHLDGLAODXASISGCPDDDAPSSLAAAATGEPAS	Db 1481 GSKPG	RTRGDGALQSLCLTTPTEEAVYCFYGNDS 1514
8NMTVLSFYLNTTVLPSSSSSRGSLDSSRSEKDRSLEREGIGLGNYHPATENPGTS	Qy 1871 DVDLSREKAELRKAKENKES .	DVDLSREKABELRKAKENKESEAKVTSHTELTSNQQSANKTQALAKQPINRGQPKPILQKQ 1930

The FANTOM Consortium,

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

the RIKEN Genome Exploration Research Group Phase I & II Team;

the Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length CDNAs.";

IN MALLE 420:563-573(2002).

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GO; GO:0005737; C:cytoplasm; IDA.

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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090; [1] ZERQUENCE FROM N.A. SERQUENCE FROM N.A. STRAILNE-CS7BL/6C; MEDLINE-22354683; PubMed=12466851; Adenomatosis polyposis g 8 g & g δ 업 ð ò $\dot{\delta}$ 9 ò 임 EDCPINNPRSGRSPTGNT -- PPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLE 2719 2776 2260 1990 GFRROLTFIKE--SPGLRRRRSELSSAESAASAPQGASPRRGR------PALPAVFLCS 2040 2230 ------VDGPSLA-----KAPIS----APFVHEGLGVAVGGFPASRHGSPSR- 2266 2377 NLTKOTGLSKNASSIPRSESASKGLNOMNNGNGA-NKKVELSRMSSTKSSGSESDRSERP 2435 2436 VLVROSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLST 2495 HSSVQ-----AGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTW 2547 AKG-TWRKIKENEF----SPINSTSQTVSSGAINGAESKTLIYQMAPAVSKTEDVWVRI 2661 1639 --- PIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQ 2376 KREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVS 2607 KKKP-SRIKGDNEKHSPRNMGGILGEDLTLDLXDIQRP---DSEHG-----LSPDSEN 2098 1683 2099 FDWKAIQEGANSIVSSIHQAAAACLSRQASSDSDSILSLKSGISLGS----PFHLTPDQ 2154 1684 VEWRAIQEGANSIVTWIHQAAA---TREASSESDSILSFVSGLSVGSTLQPPKHRKGRQ 1740 2155 EEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGOMK 2214 1741 AEGEMGSARRP-----EKRGAASVKTSGSPRSPAGPEK--------PRGT 1777 PSEGQTATTS-PRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSR 2319 PSPGQQRSRSLHRPAKTSELATISQPPRSATPPARLAKTPSSSSSQTS----PASQPLPR 1888 2194 EEVAAPKTNSSTSPSLETREPPGAPAGGO--------LSLLGSD 2720 NRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVER---TPFSSSSSKHSSPSGT STFPQSSKDIPDRGAATDEKLQ-NFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKE TEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPK ----PGVRNSSSSTSPVSKKGPPLKTPA--SKS 2777 VAARVIPFNYNPSPRKSSADSTSA 2800 -SARVPPFNYVPSPMVVAATTDSA 2289 OPLOANMPSISRGRIMIHI-----1935 2496 2548 2662 2215 2261 1833 2320 2608 1931 g & Вb 8 8 δ g ò g & g ò g δ 8 8 8 δ g ò 8 6 8 6 8 ò g & g

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649 CHSPFIHOMYSSTIPNISWRADVNSKKTIREVGSVKALMECALEVKKESTIKKSVISALWN 594
649 CHSPFIHOMYSSTIPNISWRATUPPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYMPANSYM
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                                                                                                                                                             TISSUE-Kidney,
MEDLINE-99147086; PubMed=10021369;
MEDLINE-99147086; PubMed=10021369;
van Es J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
Miles A., Kuipers J., Destree O., Peifer M., Clevers H.,
"Identification of APC2, a homoloque of the adenomatous polyposis coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 RR-GFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                416 YCETCWEWQEAHEPGMD-QDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 IAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60 MASSGOIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              239 ATEAERSSQNKHETGSHDAERQNEGQGVGEINMATSGNGQGSTTRMDHETASVLSSSSTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ----AQDRVQQTEPQALLAV------KSVPVDEDPETEVPTHPED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             53; Gaps
                                                       Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 733;
                                                                                                                                                                                                                                                                                                                                                  Miles A., Kuipers J., Destree O., Peifer M., Molenaar M., Miles A., Kuipers J., Destree O., Peifer M., Clevers H.; "Adenomatous Polyposis Coli Homologs in Mammals and Flies."; EMBL; AJ012652; CAB61207.1; "EMBL; AJ012652; AR61207.1; "InterPro; IPR000938; ARW. InterPro; IPR000255; Armadillo. Pfam. PR0014; Armadillo. Pfam. PR0014; Armadillo. Seg; 3. NON_TER 733 733
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
14.9%; Score 2172.5; DB 4; Length
Best Local Similarity 57.6%; Pred. No. 4e-99;
Matches 446; Conservative 121; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80876 MW; 09E56BE5F7032BAD CRC64;
                                                                                                                                                                                                                                                                                          Curr. Biol. 9:105-108(1999)
  protein (Fragment).
                                        sapiens (Human)
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          tumour suppressor
                                                                                                      NCBI_TaxID=9606;
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 RR-GFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLONLTKRIDSLPLTENF 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 SLQTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQ 238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 SVAPYEQLVRQVEALKAENSHLRQELRDNSSHLSKLETETSGMKEVLKHLQGKLEQEARV 63
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ы
                    LSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGTLRNVSSLIATNEDHRQ
                                                                            ILRENNCLOTILIOHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEA--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           64 LVSSGQTEVLEQLKALQMDITSLYNLKFQPP----TLGPEP---AARTPEGSPV-HGSGP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       239 ATEAERSSONKHETGSHDAERQNEGQGVGEINMATSGNGQGSTTRMDHETASVLSSSSTH
                                                                                                                                               Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison Meredith D.M.,
                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13.7%; Score 1989.5; DB 4; Length 1246; larity 30.5%; Pred. No. 9e-90; Conservative 194; Mismatches 428; Indels 697;
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                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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1.3		925 SEDESGRANQALVGTDADIKEKLEKQEEQE		1398 SRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREV 1452	1453 PKOKAPTAEKRESGPKQAAVNAAVQRVUPDADTILHFATESTPDGFSCSSSLSALSLD 1512 	1513 EPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKE-AEKTID 1558	1559 S	1573 -EILEECIISAMPTKSSRKGKKPAQTASKLPPPVARK-PSGLPVYKLLPSGNRLQPQKHV 1630	1631 SFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEPEK 1686	1687 RDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAEC	1728INSAMPKGKSHKPPRVKKIMDQVQQASASSAPNKNQLDGKK 1769 	1770 KKPTSBVKPIPQNTBYRTRVRKNADSKNNLNAER 1803 	1804 VFSDNXDSK-KQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860	1861 SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQA-IAKQPI- 1918 	1919 -NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCF 1963 : : : 1938 1578 PNQGNGNALET-ATGSKDLDSEDRSSDESNQSFIMETKYRLDSALNETCISGASEK 1636	1964	1996 QGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKK 2052	2053 PSRLKGDNEKHSPRNMGGILGEDL/TLDLKDIQRPDSEHGLSPDSENFDWKAIQEGA 2108	2109 NSIVSSLHQAAAAACLSRQASSDSDSILSLKKGI-SLGSPFHLTP 2152 	2153 DQBEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQ 2212 :
ELEREMEBHESLDRAFERGSAQQQQDEDPRANGGSSPASAGRESSKEPSTLSRPLDOD STHSAPA APPAPALLEGGAAAWITSPDERTISSAVEATIGSKVECVYSLLSWLGSNDDLEGAAKKFLEL SSGDBC_CHILNOGHAPDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCATLARGGSCAPILOQHAPADDND SGNBGCAPILARGGSCAPILOQHAPADDND SGNBGCAPILARGGSCAPILOQHAPADDND SGNBGCAPILARGGSCAPILATION SGNBGCAPILARG	-	<u>a</u> 8	g qq	è 8	& g	6 d	පු ද	ත හ	S Q	Oy Qu	충 <u>음</u>	yo,	yo, da	cy G	k a	oy G	\$ A	ठ ^व व	ර් යි	ON ON
			STHSAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAM	SSSQDSCISWRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNI IHSQPDD	SCHAGSSCATLERROCCHFLIGOGRAPHAEDNDGEVERROCHAEQALHNVVHSHFDE KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGMDQDKNPMPAEVEHQICPAVCVLMK	LSFDEERRHAMNELGELQAIAELLQVDCEMYG-LINDHYSITLRRYAGMALTNLFEDVA :	NKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALME	CALEVKKESTLKSVLSALWINSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAILES .	GGGILRNVSSLIATNEDHROILRENNCLOTLLOHLKSHSLITIVSNACGTLWNLSARNPKD	OEALWDWGAVSMLKNLIHSKHKMIAMGSAAALRNIMANRPAKYKDANIMSPG-SSI -	PSLHVRKQKALBABLDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDN : : : :	RSDNFNTGNMTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATEN	PGTSSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAH	THSNTYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRGQMKPSIESYSED	DESKFCSYGQYPADLAHKIHSANHMDDNDGBLDTPINYSLKYSDEQLNSGRQSPSQNERW	ARPKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANG :::: :::: ::::	SETURVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEEQHEEEERPTNYSIKYNEE	KRHVDQPIDYSLKYATDIP-SSQKQSF8FSKSSSGQSSKTEHMQIESBDLDISGPAGGG	NAKRONQLHPSSAQSRSGQPQKAATCKVSSINOETIGTYCVEDTPICFSRCSSLS	SLSSAEDEIG-CNQTTQEADSANTLQIAEIKGKIGTRSAEDPVSEVPAVSQHPRTKSSRL

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2304 GKSPAASRVVSGRVSSTTPPSRSNSNLNGSSAAAAAAKINQAQSRIANIWKRVDEAKTK 2363
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PINS---TSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGN 2678
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2364 OSSSNIRTQKTKSSNMLNANGTKPTLER----SSTFD------N 2397
                                                                                                                                                                                                                     ------OSP--GRNSISPGRNG----ISPPNKLS 2343
                                                                                                                                                                                                                                                                                                                       2078 AMMQQFTFITDINIGHSQETCESTDHPEDAGESPECDQMSETESCDGQEPDHLPPPPSIV 2137
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SKGLNQMNNGNGANKKVELSRMSSTKS----SGSESDRSERPV-----LVRQSTF 2443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2504 WRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVST 2563
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2259 -SKLPTKKGTA---SGGSPSK------AGSPKRIPLAPA---RRMTPQRANTSLRLAA 2303
                                                          1898 IKPPSIMDELLDSMISVDSIQSEVADGEQDCSMATTISVSNYETAACDDQTMTVLQSCFD 1957
                                                                                                                                                                                                                                                                                                                                                                      QL-----PRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESA 2397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2444 IXEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGG 2503
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRAIN=Berkeley;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
Wan K.H., Doyle C., Baxter B.G., Hell G., Nelson C.R., Miklos G.L.G.,
Abril J.F., Agbayani A., An H. J., Andrews-Pfannkoch C., Baldwin D.,
Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Drosophila melanogaster (Fruit fly).
Bukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha, Ephydroidea, Drosophilidae, Drosophila.
                  MKQP-----LOANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPL-
                                                                                                         -----KTPASKSPSEGQTATTSPRGAKPSVKSEL-----
                                                                                                                                                                                                                                                                                                                                                                                                                   DLRTSVVKPTTLEPATAVKLVRGRKKPAYVSPYSMQSQRN---
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Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dallke C., Davenport L.B., Davies P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Dosler C., Gabriellan A.B., Gargn N.S., Galbart W.M., Glasser K.,

RA Fosler C., Gabriellan A.B., Gargn N.S., Galbart W.M., Glasser K.,

RA Harris N.L., Harvey D., Heiman T.J., Hermandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Hermandez J.R., Houck J.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

Alali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., McLeod M.P., Moshrefi A.,

Alasko P., Lei Y., Levitsky A.A., Li J. J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J. J., Li Z., Liang Y., Lin X.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., J. J., S., P., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzhy D.M., Nollson D.L.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Rese M.G.,

RA Rainert K., Remington K.A., Nixon K., Nusskern D.R., Parlb J.M.,

Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Shith T.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Shiskas R., Tector C., Turner R., Wang A.H., Wang A.H.,

RA Spier E., Spradling A.C., Stapleton M., Strong R., Shik S., Mulliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Shiskas R., Tector C., Turner R., Wang A.H., Wang A.H., Wang X.,

RA Shiskas R., Tector C., Turner R., Vanner E., Wang A.H., Wang S., Yao Q.A.,

RA Shiskas R., Tector C., Stapleton M., Strong R., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., Shik M., S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             243 ERSSQNKHETGSHDAERQN-EGQGVGEINMATSGNGQGSTTR------MDHETASVLSSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       296 STHSAPR------RLTSH-----LGTKVEMVYSLLSMLGTHDKDDMSRTLLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               515 NKATLCSMKGCNRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LSFDEEHRHAMNELGGLQAIAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA
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12.1%; Score 1763; DB 5; Length 2417;
Best Local Similarity 25.3%; Pred. No. 3.4e-78;
Matches 720; Conservative 326; Mismatches 836; Indels 964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR008938; ARM.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 5.
SMART; SM0108; ARM; 5.
PR05ETI; PS50176; ARM; REPEAT; 2.
SEQUENCE 2417 AA; Z61282 MW; 08327727C475F254 CRC64;
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1685	1298	1728 .	1358 8	1768 1	1418	1802 F	1478 E	1859 1	1524	1919 .	1564 I	1959	1623 [1981	1678 P	2038 I	1719 8	2094 F	1776 E	2141	1836	2198 I	1885 -	2253 I	1944 7	2283 -	2004 1	2322	2064	2334 N	2124	2383 (2179	2437	2217 E
ò	Dp	ò	Dp	ò	q _Q	à	ОЪ	ò	qq	ò	셤	ò	qq	&	qq	ò	qa	δ	qq	ΟŊ	QQ	δλ	Db	δy	QQ	ò	QD	à	qu	ò	DÞ	ò	Db	δ	qq
530 AGGILRNVSSHIAVCEPYRQILRQHNCLAILLQQLKSESLTVVSNSCGTLWNLSARSAED 589	OBALWDWGAVSMLKNLIHSKHKMIAMGSAAALRNIMANRPAKYKDANIMSPG-SSL	QXFLWDNGAVPMLKSLIHSKHAMISEGSSSALKNLLLNFRFAVQNHQLDFITAKSMGLKAL	750 PSLHYRKOKALEAELDAQHLEETFDAIDNLSPKASHRSKORHKQSLYGDYVFDTNRHDDN 809 	METHOD TO TO DESCRIPTION OF THE PROPERTY OF TH		CO HEADOGGIANGAGATAN HITTESSOS GUGOSTHIAS VARIANINA I O A STIPLE I O ISOS CONTRA LA STIPLE I O ISOS CONTRA LA CARRETA DE LA CARR		THSNITYNFIKSENSNRICSMPYAKLEYKRSSNDSINSVSSNDGYGKRGOMKPSIESYSED	: : : : AHR	990 DESKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERW 1049	: :	ARPKHIIEDEIKOSEOROSRNOSTTYPVYTESTDDKHLKFOPHFGQOECVSPYRSRGANG	:::	SETURVGSNHGINONVSOSLCOEDDXEDDKPTNXSERYGEBROHERBRPTNYSIXXNEE			ACHAVICATORIALIDIS SOCIOS SOCIEDAS SOCI	O TOOM OF THE COMPANY AND THE	NAME OF THE PROPERTY OF THE PR	TOO QUARRANTO STANDARD A COMMON TO STANDARD A COMMON TO STANDARD AND S	12/9 SESSMEDELG-CNQTIQEADSANILGIAEIRCALGIRSAEDFVSEVFAVSQRFRIASSAL 1337		COSDESSIONATORANDE POGRACI PONDOMO I FANDE PERI I COLLEGIO NO COLLEGIO NE COLL	O TOTAL OCCIONADO CONTROL TOTAL DE CONTROL D	0.001A0.00400000000000000000000000000000	PKNKAPTAEKRESGPKOAAVNAAVORVOVI.PDADTI.I.HFATESTPDGFSCSSSI.SAL.SL-	PRRNSVAGSGONVDSPPVVIPASLOPLRSVFE-DDLSSFNVEHTPAGFSTATSLSNLSIV	-DEPFIOXDVELRIMPPVOENDNGNETESEQPKESNENOEKE-AEKT		בחיים ביים ביים ביים ביים ביים ביים ביים	DOUGHER TO TOUR WAS A CONTRACT TO A CONTRACT	INGICIEDIRADESAVEONINESVIONIOSIDENALMAQAQMIANIQUEDDVOSNASDUGG	15.5	ANGELLINGS CANDEST CONTRACT TO THE MODIFICATION OF THE PROPERTY AND THE PROPERTY OF THE PROPER	1649 HVSFTFGDDWEKVICVEGIFINFSTAISLSDDIILESFRNELAAGEGVKGGAGGGEF 1884
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1685	EKRDTIFTEGRSTDEAGGGKTSSVIPELDDNKABEGDILAEC1727
1298	KAKPGKQEQVRRPPHWQDDSLSSLSIDSEDDTNLLSQAİAAGCNRFKSNLGFSSNGKRSS 1357
1728	INSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDG 1767
1358	SLSSSQPIAINAATSASSLNSAMTVRKSQQQESYSSVDSSDSNDNQSKSLFELCILKGMY 1417
1768	KKKKPRPVKPIPQNTEYRTRVRKNADSKNNLNA 1801
1418	KTKEPGARAQQMQEQPIVGSSSVQSNPSLKQFDSLPVQLPSSGQVKRQRHHHHHHHHRER 1477
1802	ERVFSDNKDSK-KQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSR 1858
1859	ANKTOAIAKOP
1524	- TSASALSTAAPDVEQKAHATSNPQQQSSTHPSSHILPNPI 1563
1919	NRGOPKPILOKOSTPPOSSKDIPDRGAATDEKLONFAIEN 1958
1959	IPVCFSHNSSLSSLSDIDQENN 1980
1623	QLRS
1981	NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD 2037
1678	vsotapv
2038	SSAMPKKKKDSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLS 209
1719	LNFQLGGQVQNAGVRLE 177
2094	PDSENFDWKAIQEGANSIVSSLHQAAAACLSRQASSDSDSILSLKS 2140 : : : :
2141	GI-SLGSPFHLTPDQEEXPFTSNKGPRILKPGEKSTLETKKIBSESKGIKGGKKVYKS 2197
1836	
2198	LITGKVRSNSBISGQMKQPLQANMPSISRGRIMIHIPGVRNSSSSTSFVSKKGPP 2252
1885	LMD
2253	L 2282
1944	SAES
2283	SPVARQTSQI2321
2004	YTIATSCEMEAPEANETLOIEIVEAAVEVATPSFRANGRRRGSAERYKTÖLIECPLALIQ 2063
2322	
2064	PQPDDCPSEQLSSIRAMMQQFTFITDINIGHSQETCESTDHPEDAGESPECDQNSETESC 2123
2334	LTKQT 23
2124	GOEPDOLPPPS
2383	LSKNASSIPRSESASKGLNQMNNGNGANKKVELSRMSSTKSSGSESDRSERPV- 243
2179	221
2437	APSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSL 248
2217	PPEPAPARLERQGTFVKDEPINSNVQVPVVE-TK 2249

933 -NTYNFTKSENGNRTCSMPYAKLEYKRSSNDSLNSVSSNDGYGKRQ@MKPSIESYSEDDE 991	SKFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGROSPSQNERWAR	325ECPLA 339 1052 PKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSE 1111	RCGQPRPSR	1112 TNRVGSNHGINQNVSQSLCQEDDYEDDEPTNYSFRYSEBEQHEBEERPTNYSIKYNEEKR 1171 112 TNRVGSNHGINQNVSQSLCQEDDYEDDEPTNYSFRYSEBEQHEBEERPTNYSIKYNEEKR 1171 349LDLDLDLPGCQAEPPAREATSADARVRTIKLSPTYQ 382	HVDQPIDYSLKYATDIPSSQXQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRQNQL	HVSPGARRQABPLAGPGISPGARRQAWL	1232 HPSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSAEDELGCNQ 1291 13	1292 ITQEADSANTLQIAEIKGKIGTRSAE-DPVSEVPAVSQHPRTKSSRLQGSSLSSESARHK 1350	469 GGDLDDSDSSLEGLEEAGPSEAELDSTWRAPGATSLP505	AVEFPSGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESKSIASSVQS	-VALPAPRRNKGRGLGVGDATPSSSSENYVQETPLVLSRUSSVSSLGSFESFSTASSLFS	1408 BPCSGAVSGIISPSDLPDSPGQTMFPSRRKTPPPPPQTAQTKREVPKNRAPTAEKKES 1465 	1466 GPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKDVEL 1522	618 YVKRFLDIADCRERCRLPSELDAGS-VRFTVEKPDENFSCASSLSALALHEHYVQQDVEL 676	RIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSEKDLLDDSDDDIEILEECIISA	RLLPSACPERGGGAGGAGLHFAGHRRREEGPAPTGSRPRGAADQELELLRECLGAA	1583 MPTKSSRKGKKEAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTFGUDMEKVY 1642 - - - - - - - - - - - - -	CVEGTPINESTATSISDIJIESPPNEIAAGEGVEGGAGGEFEKRDIJPTEGRSTDEAGG	SAEGTEVNFSSAASLSDETLQGPPRDQFGGPAGRQRPTGRPTSARQA	GKISSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSAPNK	821AGGAGKOREG 850	SEGAGRARAGLELPLGRPPSAPA	ONLKNNSKDENDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVD	866 PG		1934 PQSSKDIPDRGAATDEKLQ-NFALENTPVCFSHNSSLSSLSDIDQENNNKENZPIKETEP 1992 	
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Qy 2489 PDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWK 2548 : : : : :	QY 2549 REHSKHSSSLPRVSTWRRTGSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSA 2608	OY 2609 KGTWRKIKENEFSPTNSTSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIED 2663		Db 2398NTPSTAGGVKSK 2409	SULT 10 UEM8	Q9UEM8 PRELIMINARY; Q9UEM8;	AY-2000 (AY-2000 (ZT-2003 (OS HOMO Sapiens (numan). OC Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia: Bulberia: Primitea: Catarrhin: Hominidae: Homo					EMBL; AUISII8/; CAAIOSI/.1; GO; GO:0005578; C:extracellular matrix; IEA. GO: GO:0000202: E:metalloandaridane activity.	DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA. DR InterPro; IPR008938; ARM.			SEQ	Query Match 11.7%; Score 1705; DB 4; Length 1685; Best Local Similarity 28.4%; Pred. No. 1.5e-75; Matches 636; Conservative 271; Mismatches 672; Indels 660; Gaps 85;	OLLRENNCLOFILOHLKSHSLTIVSNACGTUMLSARNPKDORLWDWGAVSMLKNLHS 7	Db 1 GVLRDHNCLQTLLQHLTSHSLTIVSNACGTLWNLSARSARDQELLWDLGAVGMLRNLVHS 60	Qy 714 KHKMIAMGSAAALRNIMANRPAKYK-DANIMSPGSSLPSLHYRKQKALBAELDAQHLSET 772 Dh 61 KHKMIAMGSAAALRNIMAHDAKHOAAATARFOGS (WYDSCAALBAELDAGHLAGET 772)	9.1 MINGTENDOSFRANDLANDERSKYANDERSKY OF 950 VESTE VANKKATURKA 773 FDNI DNLSPKASHRSKQFRKQSLYGDYVFDTNRHDDNRSDNFNTG	Db 121 LEHLEKQGPPAAEAATKKPLPPLRHLDGLAQDYASDSGCFDDDDDAPSSLAAAAATGBPAS 180	CY 818NMTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTS 873 - 181 paalesiptoseptoroniaptoppole companies (181 paalesiptoseptoroniaptoroniaptoppole companies (181 paalesiptoseptoroniaptoppole companies (181 paalesiptoseptoroniaptoro	874 SKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHS-	Db 223 AKAKAKLALAVARIDQLVEDISALHTSSDDSFSLSSGDPGQEAPREGRAQSCSP 276

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                                       DECURINE 2235468; PubMed=12466851;
MEDLINE=2235468; PubMed=12466851;
The FANTOM Consortium,
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I annotation of
"Analysis of the mouse transcriptome based on functional annotation of
60,770 full-length cDNAs.";
Nature 420:563-573(2002).
EMBL; AR0803724; BAC38887.1; -.
SEQUENCE 324 AA; 36909 MW; D74E29ECD952DICC CRC64;
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Bukaryota, Metazoa, Arthropoda, Hexapoda; Insecta, Pterygota,
Neoptera, Endopterygota; Diptera; Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
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Pred. No. 5.3e-54;
9; Mismatches 14
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Best Local Similarity 91.0%;
Matches 253; Conservative
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APC2 OR E-APC OR CG6193.
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                             PAVHPRGREPAVT-------KDPGPGGRDSSPSP---RAAEELLQRCISSALPRRRP 1024
                                                                                                                                                                                                                                                   RAIQEGANSIVTWLHQAAAA---TREASSESDSILSFVSGLSVGSTLQPPFKHKGRQAEG 1125
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                                                                                                                              KAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGS----PFHLTPDQEEK
                                                                                                                                                                                                                                                                                                     PFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPL
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                                                                                                 P-SRIKGDNEKHSPRNMGGILGEDLTLDLKDIQRP---DSEHG----LSPDSENFDW
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NCBI_TaxID=10090;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adenomatosis polyposis coli.
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PVSGLR----RRKPR-
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1385 RVKKIMDQ-----VQQASASSSAPNKNQLDGKKKKRPTSPVKPIPQNTEYR 1786 RQNQLHPSSAQSR-----SGQPQKAATCKVSSINQETIQTYCVF 1265 1499 LDEPFIQKDVELRIMPPVQENDNGNETESEQFKESNENQE-KEAEKTID 1558 1611 RLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAA 1671 IIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYR 1103 VGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSBEEQHEEFFRPTNYS 1163 SSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSP 1043 887 9 DIPEQKPSTVFE------DIVINREHUBAN 750 841 505 482 483 426 923 470 KKOKALEAELDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDT 803 863 432 983 BVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDG LQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQETPLMFS У-----#IGNMTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNY -----STKYST-----

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                                               1731 AMPKGKSHKPFRVKKIMDQ-----VOQASASSAPNKNQLDGKKKKPTSPVKPIPONTEYR 1786
                                                                                                                                        1787 TRVRKNADSKNNLNAERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHY 1846
                                                                                                                                                                                                                                                                530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 ALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNE 180
                                                                                                                                                                      9
----GSAKAGPVLK---LPM--RTAEEAQA------PKLPPRRSAVQGD----AEP 924
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 GLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 AQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMSCALBVKKBSTLKSVLS
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                                                                                                                                                                                                                                  1847 TPIEGTPYCFSRNDSLSSLDFDDDDVDLSREK-----AELRKAKENKESEA----
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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01-0cT-2000 (TrEMBLrel. 15, Last sequence update)
01-0cT-2003 (TrEMBLrel. 25, Last annotation update)
Adenomatosis polyposis coli tumor suppressor (Fragment)
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208 AA; 22726 MW; 51076F257B61C528 CRC64;
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100.0%; Pred. No. 5.4e-44;
Attive 0; Mismatches 0;
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Hum. Genet. 106:101-107(2000).
EMBL; AF127034; AAF34355.1; -.
INTERPO: IPRO08938; ARM.
INTERPO: IPRO00225; ARMadillo.
PFAM; PFO0514; Armadillo.seg; 2.
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Su L.K., Steinbach G., Sawyer J.C.,
"Genomic rearrangements of the APC
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PRELIMINARY;

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REDLINE-22388257, PubMed=12477932;

MEDLINE-22388257, PubMed=12477932;

A traubberg R.L., Feligold E.A., Grouse L.H., Derge J.G.,

A traubberg R.D., Collins F.S., Wagner L., Sheamen C.M., Schuler G.D.,

A ltschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,

A ltschul S.F., Zeberg M.B., Moore T., Max S.I., Wang J., Haieh F.,

A papleton M., Soares M.B., Bonaldo M.F., Casvannt T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villaion D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Mhiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Redriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Rrywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

T. "Generation and initial analysis of more than 15,000 full-length human man mouse orbx sequences."
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01-OCT-2003 (TrEMBLrel. 25, Created)
1-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Hymo sapiens (Human).
Eukarosapiens (Hordata, Craniata, Vertebrata, Butele
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056268; AAH56268.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  159 AA; 17843 MW; E0C0CC055A22C91B CRC64;
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

August 25, 2004, 16:58:01; Search time 180.5 Seconds (without alignments) 4450.319 Million cell updates/sec Run on:

US-09-442-489F-2 14575 1 MARASYDQLLKQVEALKMEN......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score:

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Scoring table:

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1586107 segs, 282547505 residues Searched:

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Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

A Geneseq 29Jan04:* 1: geneseqp1980s:* geneseqp1980s:* geneseqp1990s:* Database

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	2 APC ge	Aaw35392 Human ade	Aaw38370 Human ade	Abg90964 Human ade	7 Adenog	Aaw76140 Human APC	4 Human	Aab23011 Human APC	5 Human	Aaw76821 Human APC	- N	4	4	Aar63508 Adenomato	œ	Aaw11922 Adenomato	Ade65846 Human ade	2 Huma	Ade56175 Rat Prote	Abg71106 Human ade	Human	Aab50674 Mouse APC	Abg09335 Novel hum	18 Human	Aay92061 Human APC
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AAY92060	ABB58126	AAR88353	ABB62156	AAU37120	ABB68397	ABB66878	ABB67502	ABU16000	ABM72734	ABP56876	AAB50654	ABJ18914	AAW33894	AAW82368	ABP39618	ABB60327	ABB60291	ABB65772	ABB71160
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12.1	12.1	10.1	8,4	3.8	3.7	3.6	3.6	3.6	3.6	3.6	3.5	3.5	9.5	3.5	3.4	3.4	3.3	3.3	3,3
1767.5	1763	1478	1221.5	556.5	53	526.5	524.5	518	517.5	517.5	516.5	514.5	507.5	507.5	93.	4	481.5	474.5	474.5
26	27	28	53	30	37	32	33	34	35	36	37	38	გ	40	41	42	43	44	45

ALIGNMENTS

neoplasm; cancer; oncogene; tumour; growth; detection; diagnosis; prognosis; treatment; sporadic colorectal carcinomas; ss. APC gene product in familial adenomatous polyposis. AAR26052 standard; protein; 2843 AA. (revised)
(first entry) 25-MAR-2003 28-JAN-1993 AAR26052; RESULT 1 AAR26052

Homo sapiens. WO9213103-A1. 06-AUG-1992.

(UYJO) UNIV JOHNS HOPKINS. (ICIL) INPERIAL CHEM IND PLC. (UTAH) UNIV UTAH. (CANC-) CANCER INST. 91GB-00000963. 91US-00741940. 92WO-US000376. 16-JAN-1992; .6-JAN-1991; 08-AUG-1991;

White RL; Markham AF; Thliveris A, Anand R, Hedge PJ, I Groden JL, Joslyn G, Vogelstein B, Carlson ML, Kinzler KW, Albertsen H, Nakamura Y;

WPI; 1992-284685/34. N-PSDB; AAQ27234.

Detection of somatic and germ-line alterations of human APC gene - used to diagnose, treat and study familial adenomatosus polyposis and sporadic colorectal cancer.

Disclosure; Page 47; 132pp; English.

This sequence is encoded by the APC (Adenomatous Polyposis Coli) generassociated with tumorigenesis, found on chromosome 5q. The sequence may be mutated by deletions insertions, investions, or point mutations of the gene . The APC gene is expressed in most normal tissues as well suggesting that APC is a tumour suppressor. (Updated on 25-MAR-2003 to correct PN

961 NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE 1020 1021 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE 1080 1021 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE 1080 1081 STDDKHLKFOPHFGQDECVSPYRSRCANGSETNRVGSNHGSINQNYSQSLCQEDDYEDDKP 1140 1081 STDDKHLKFQPHFGQOECVSPYRSRCANGSETNRVGSNHGINQNYSQSLCQEDDYEDDKP 1140 1081 STDDKHLKFQPHFGQOECVSPYRSRCANGSETNRVGSNHGINQNYSQSLCQEDDYEDDKP 1140 1141 TNYSERYSEBEQHEBEERPTNYSIKYNESKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS 1200 1141 TNYSERYSEBEQHEBEERPTNYSIKYNESKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS 1200 1141 TNYSERYSEBEQHEBEERPTNYSIKYNESKRHVDQPIDYSLKYATDIPSSGKQSFSFSKS 1200	1201 SSGQSSKTEHMSSSSENTSTPSSNAKRONQLHPSSAQSRSGOPOKAATCKVSSINOETIQ 1260	1321 SEVPAVSQHPRTKSSRLQGSSLSSBSARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQET 1380	1441 PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVOVLPDADTLLHPATESTPDGF 1500 1441 PPPQTAQTKKEVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 1500 1501 SCSSLSALSLDEPPIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKRAEKTIDSE 1560 1501 SCSSSLSALSLDEPPIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKRAEKTIDSE 1560 1501 SCSSSLSALSLDEPPIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1560 1501 SCSSSLSALSLDEPPIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1560	1561 KDLLDDSDDDIEILEECIISAMPTKSSRKGKKBAQTASKLPPPVARKESQLPVYKLLPS	1681 SGEFEKRDTIPTEGRSTDEAQGKTSSVTIPELDDNKAEBGDILAECINSAMPKGKSHKP 1740 [1801 AERVFSDNKDSKKQNLKONSKDFNDKLPNNEDRYRGSFAFDSPHHYTPIEGTPYCFSRND 1860 1801 AERVFSDNKDSKKQNLKONSKDFNDKLPNNEDRYRGSFAFDSPHHYTPIEGTPYCFSRND 1860 1861 SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR 1920 1861 SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR 1920 1861 SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR 1920	1921 GQPKPILQKGSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDGENN 1980 1921 GQPKPILQKGSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSIDGENN 1980 1981 NKENEPIKETEPPDSGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 1981 NKENEPIKETEPPDSGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 1981 NKENEPIKETEPPDSGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 2040 2041 ECISSAMPKKKKFSRLKGDNEKHSPRNMGGILGEDLTDLKDIQRPDSEHGLSPDSENFD 2100
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field.) (Updated on 25-MAR-2003 to correct PI field.) Sequence 2843 AA; ery Match ery Match st Local Similarity 100.0%; Pred. No. 0; tches 2843; Conservative 0; Mismatches 0; Indels 0; Gaps 0 1 MAAASYDOLLKQVEALKMENSNLROELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 60	RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFEL RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT	2 H-H H-F	HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQEDDKRGRREIRVLHLLEQIRAYCETC 4 HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQEDDKRGRREIRVLHLLEQIRAYCETC 4 HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQEDDKRGRREIRVLHLLEQIRAYCETC 7 WEWQEAHEPGMDQDKNPWPAPVEHQICPAVCVLMKLSFDEEHRHANNELGGLQAIAELLQ 4 HGHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIHIH		ENKADICAVBGALAFLYGTLTYRSQTWTLAIIESGGGILRNVSSLIATWEDHRQILRENN 6 ENKADICAVBGALAFLYGTLTYRSQTWTLAIIESGGGILRNVSSLIATWEDHRQILRENN 6 ENKADICAVBGALAFLYGTLTYRSQTWTLAIIESGGGILRNVSSLIATWEDHRQILRENN 6 CLOTLLOHLKSHSLITVSNACGTLWNLSARNPKDQBALWDMGAVSMLKNLIHSKHKMIAM 7 CLOTLLOHLKSHSLITVSNACGTLWNLSARNPKDDRALWMGAVSMLKNLIHSKHKMIAM 7	GSAAALRNLMANRPAKYKDANIMSPGSSLPSCHYRKOKALEAELDAQHLSETFDNIDNLS 78 GSAAALRNLMANRPAKYKDANIMSPGSSLPSCHYRKOKALEAELDAQHLSETFDNIDNLS 78 GSAAALRNLMANRPAKYKDANIMSPGSSLPSCHYRKOKALEAELDAQHLSETFDNIDNLS 78 PKASHRSKORHKOSLYGDYVPDTNRHDDNRSDNFNTGNMTVLSPYLNITVLPSSSSRGS 84 PKASHRSKORHKOSLYGDYVPDTNRHDDNRSDNFNTGNMTVLSPYLNITVLPSSSSRGS 84 PKASHRSKORHKOSLYGDYVPDTNRHDDNRSDNFNTGNMTVLSPYLNITVLDSSSSSRGS 84	LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEVSAIHTS 90 LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEVSAIHTS 90 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 96

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The present sequence is the human adenomatous Polyposis coli (APC) gene product, which was used in the development of a novel method of diagnosing or prognosing an APC gene associated neoplastic tissue. The method comprises comparing APC gene coding sequences or mRNA in a tumour tissue, to APC gene coding sequences or mRNA in a non-neoplastic tissue, tumour tissue. APC is a tumour repressor expressed in most normal tissues. APC mutations are found in familial adenomatous polyposis and sporadic colorectal cancer patients. The method enables mutations to be detected to provide an indication of predisposition to cancer. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                           Cancer diagnosis - by detecting mutation(s) in adenomatous polyposis
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Vogelstein B, Thliveris A, Anand R,
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1501 SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1560 	1561 KDLLDDSDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKFSQLPVYKLLPS 1620 	1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680 1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680	∞ — ∞	1741 FRVKKIMDQVQQASASSSAFNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLN 1800 	1801 AERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHYTPIEGTPYCFSRND 1860 	SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELISNQOSANKT 	1921 GQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQENN 1980 	1981 NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 2040	2041 ECISSAMPKKKRPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100	2101 WKAIQEGANSIVSSLHQAAAAACLSRQASSDSSILSLKSGISLGSPFHLTPDQEEKPFT 2160 	2161 SNKGPRILKPGEKSTLETKKIESESKGIKGCKKVYKSLITGKVRSNSEISGQMKQPLQAN 2220 	2221 MPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280 2221 MPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGGTATTSPRGAKPSVKS 2280		2341 KLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKG 2400 	2401 INQMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESA 2460 	2461 SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG 2520	2521 RPAKKHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES 2580	81 SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSGTV6
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421 WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVIMKLSFDEEHRHAMNELGGLQAIAELLQ 480 	VDCEMYGLTNDHYSITLRRYAGMALTNITPGDVANKATLCSMKGOWRALVAQLKBESEDL 54 VDCEMYGLTNDHYSITLRRYAGMALTNITPGDVANKATLCSMKGOWRALVAQLKBESEDL 54 VDCEMYGLTNDHYSITLLSRYAGMALTNITPGDVANKATLCSMKGOWRALVAGLKEREPDL 54	QOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT 6		7 7	NIDNLS 78	SSSRGS 84	SAIHTS 9	OEDRSGGSTTELHCVTDERNALRRSSAAHTHSNITWPTKSENSNRTCSNPYAKLEYKRS 96 OEDRSGGSTTELHCVTDERNALRRSSAAHTHSNITWPTKSENSNRTCSNPYAKLEYKRS 96 OEDRSGGSTTELHCVTDERNALRRSSAAHTHSNITWPTKSENSNRTCSNPYAKLEYKRS 96	NDSLNSVSSNDGYGKRQQMKP8 ESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE	YPVYTE	STDDKHLKFQPHFGQQECVSPYRSRCANGSFTNRVGSNHGINQNVGQSLCQEDDYEDDKP 114 STDDKHLKFQPHFGQQECVSPYRSRCANGSFTNRVGSNHGINQNVGQSLCQEDDYEDDKP 114 STDDKHLKFQPHFGQQECVSPYRSRCANGSFTNRVGSNHGINQNVGQSLCQEDDYEDDKF 114	TNYSERVSEEGHEEERPTNYSIKYNEEKHVDOPIDYSIKYATDIPSSOKOSFSFSKS 120	SSGQSSKTEHMSSSENTSTESSNARRQNQLHPSSAQSRSGQPQKAATCKVSSINOETIQ 126	SAEDPV 1	SEVPAYSOHPRIKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQIPKSPPHYVQET 138 SEVPAVSOHPRIKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQIPKSPPHYVQET 138 SEVPAVSOHPRIKSSRLQGSSLSSESARHKAVFFPSGAKSPSKSGANIPKSPPHYVQET 138	PIMPERCIANS PIMPERCIANS	PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 150	STPDG

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Hedge PJ, Carlson M, Anand R, Thliveris A, Albertsen H, White
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          tissues. APC mutations are found in familial adenomatous polyposis and sporadic colorectal cancer patients. The method enables mutations to be detected to provide an indication of predisposition to cancer. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                           181 QIDLTRRQLEYEARQIRVAMEEQLGTCQDMEXRAQRRIARIQQIEKDILRIRQLLQSQAT
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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2843; Conservative 0; Mismatches
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QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE STDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP

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PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP

1441 PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQKVQVLPDADTLLHFATESTPDGF SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE

PPOJTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF

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KOLLODSODDIELLEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPS

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1561 KDLLDDSDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPS

SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE

2401 2461 2461

2401

LINGMANGNGANIKKVELSRASSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESA

2341 KLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKG INOMINGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESA

2341

SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG

SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG

2521 RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES

RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES

2521

2581

2581 SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPINSTSQTVSSGATNGAES

KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN

2641 2701

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SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES

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> DSTESSGTOSPKRHSGSYLVTSV 2843 Ą 2843 ABG90964 standard; protein; entry) (first 29-NOV-2002 2821 CC

> > AERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860

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AERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR GOPKPILOKOSTFPOSSKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENN

1741 FRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLN

FRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLN

SGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP

1681 1741

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PFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQI PTPVNNNTKKRDSKT

DSTESSGTQSPKRHSGSYLVTSV 2843

2821

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2761

PFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSKT

QAKQNVGNGSVPMKTVGLENRLTSF1QVDAPDQKGTEIKPGQNNPVPVSETNBSPIVERT 2701 QAKQNVGNGSVPMRTVGLENRLISFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERT

Adenomatous polyposis coli; APC; human; neoplastic tissue; mutation detection; tumour; cancer. protein #1. Human adenomatous polyposis coli (APC)

1980

NKENBPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 2040

GOPKPILOKOSTFPOSSKDI PDRGAATDEKLONFAIENTPVCFSHNSSLSSLSDIDOENN

Method to aid in the diagnosis/prognosis of neoplastic tissues in humans, by detecting somatic alteration of wild-type APC protein in tumor tissue isolated from human, the alteration indicating neoplasia of the tissue. Hedge PJ, Groden J, Hedg , Thliveris A, Carlson M, G Nakamura Y, JAPANESE FOUND CANCER RES Disclosure, Fig 3, 140pp, English 91GB-0000962. 91GB-0000963. 91GB-0000974. 91GB-0000975. 91US-00741940. 95US-00449731 JOHNS HOPKINS. UTAH. Anand R, Markham AF, WPI; 2002-641559/69. N-PSDB; ABS67119. ZENECA LTD Albertsen H, Kinzler K, Ma White RL; 16-JAN-1991; 16-JAN-1991; 16-JAN-1991; 16-JAN-1991; 08-AUG-1991; 12-AUG-1991; VINU US6413727-B1 25-MAY-1995; 02-JUL-2002 (UYJO) (UTAH) (NICA-) (ZENE)

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e PJ, Joslyn Vogelstein B;

This invention relates to a novel method to aid in the diagnosis or prognosis of a neoplastic tissue of a human. The method involves detecting somatic alteration of wild-type adenomatous polyposis coli) protein in a tumour tissue isolated from a human (the alteration indicating neoplasia of the tissue). The method of the invention is method is useful in diagnosis or prognosis of a neoplastic tissue of a human. the method is useful in detection of genetic predisposition to cancer. The present sequence represents a protein sequence used in the method of the invention

Sequence 2843 AA

ö 120 180 240 240 EAERSSONKHETGSHDAERQNEGGGVGEINMATSGNGGGSTTRMDHETASVLSSSSTHSA 300 PRRLISHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 360 360 120 180 HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC 420 09 9 QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDIJRIRQLLQSQAT PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTTLLAMSSSODSCISMROSGCLPLLIQLL 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM ASSGQIDLLERLKEINLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR RGFVNGSRESTGYLBELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM ASSGOIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR Gaps ö Length 0; Indels 5; DB Score 14575; ; Pred. No. 0; 0; Mismatches 100.0%; Best Local Similarity 100. Matches 2843; Conservative 61 61 121 121 181 181 241 241 301 301 361 Query Match 8 6 8 8 8 8 8 8 8 8 a

1080 1020 480 480 540 009 900 099 999 720 720 780 780 840 840 900 900 096 960 PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF STDDKHLKRQPHFGQQECVSPYRSRGANGSTNRVGSNHGINQNVSQSLCQEDDXEDDKP SSGOSSKTEHMSSSSENTSTPSSNAKRONOLHPSSAQSRSGOPOKAATCKVSSINOETIO SSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHFSSAQSRSGQPQKAATCKVSSINQETIQ TYCVEDTPICESRCSSLSSAEDEIGCNOTTORADSANTLQIAEIKGKIGTRSAEDPV HGNDKDSVLLGNSRGSKEARARASAALHNI HSQPDDKRGRREIRVLHLLEQIRAYCETC WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL 541 QQVIASVLRNLSWRADVNSKKTLRBVGSVKALMECALEVKKESTLKSVLSALMNLSAHCT ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS GSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALBABLDAQHLSETFDNIDNLS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIISDEIKQSEQRQSRNQSTTYPVYTE LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE TNYSERYSEEEQHEEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQET PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP PLMFSRCTSVSSLDSFESRSIASSVOSEPCSGWVSGIISPSDLPDSPGGTMPPSRSKTPP WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALMNLSAHCT ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS OEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS SIDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP TNYSERYSEEEQHEEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKS TYCVEDTPICESRCSSLSSAEDEIGCNOTTOEADSANTLOIAEIKGKIGTRSAEDPV SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKSPSKSGAQTPKSPPEHYVQET 421 901 961 1021 1021 1081 1141 1201 1201 1261 1261 1321 1381 1381 1441 361 481 481 541 601 601 781 781 841 841 196 1081 1141 1321 661 661 721 721 901 ^& A 9 ð g ò g ò 엄 ò 임 ò g ઠે 8 8 a ò 셤 ò g ò q ò g δ g 8 g 8 g 8 <u></u> 8 ò .. <u>ದ</u>

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                                                                                                                    2701 QAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKFGQNNPVPVSETNESPIVERT
                                                                                                                                                                                                                                                                           PFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIFTPVNNNTKKRDSKT
                SEKAKSEDEKHVNSISGTKOSKENQVSAKGTWRKIKENEFSPINSTSQTVSSGATNGAES
                                           2581 SEXAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
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                                                                                             KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Anand R, Nakamura Y, Groden J, Kinzler
, Vogelstein B, Albertsen H, White RL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adenomatous polyposis coli; tumour repressor; Gardner's syndrome; familial adenomatous polyposis; cancer diagnosis and prognosis; tumorigenesis suppression.
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91GB-00000963.
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Carlson M,
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N-PSDB; AAQ72297.
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Thliveris A,
Joslyn G;
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PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 1500
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                                                            QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ
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                                       SCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE
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cancers such as familial adenomatous polyposis (FAP) and Gardner's 8×386666666888

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he wild type APC gene (or a part of it) ally to restore gene function, while pri m the cDNA (AAQ7233-400 and AAQ7251-56 tions. Also APC proteins or analogues cafor a defective gene, and epithelial cel rying a mutated APC allele are useful foagants able to suppress tumorigenesis. rect PA field.)	99.8%; Score 14551; DB 2; Length 2860; Similarity 99.4%; Pred. No. 0; 2; Conservative 0; Mismatches 0; Indels 18;	AAASYDOLLKQVEALKMENSNIRQELEDNSNHLTKLETEASNMKEVIKQLQGSIEDEAMA 61 	SNFPGVKLRSKMSLRSYGSREGSV 1	SGQIDLLEKLKELNIDSSNYPGVALKSANDLKSIGSNYPGVALKSANDLKSLKSIGSNEGGG 7.12 SRSGEGSPVPMGSPPRRGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDMYYAQLQ 16	RGGECSPVPMGSFPRGFVNGSRESTGYLEELEKERSLILADLDKEEKEKD	NLTKRIDSLPLTENFSLGTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAGRRIARIÇQ 223 	ATEAE	ILRIRQLLQSQATEAERSSQNKHETGSHDAERQNEGQGVGEINMATSGN	MDHETASVLSSSSTHSAPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDS 343 	CISMROSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRRE 403	VLHILEOIRAYCETCWEWOEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHR 46		HAMNELGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMK 52	HAMNELGGLLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMK 54	GCWRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKES 583 	TLKSVLSALMNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIESGGGTLRNVS 6	TEKSVESALMNESAHCTENKADICAVDGALAFEVGTETYRSGTNTLAIIESGGGILRNVS 6	SLIATNEDHROI	SLIAINEURKŲ LEKENNCLŲ LELQRIANGROLI VONACGI LANGARNIS KARPARITOROS. 72	VSMLKNLIHSKHK	17-	LDAQHLSETFDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLS	1 PYLNITYLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTT 883
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ò	04	ANHMDDINGELDTPINYSLKYSBBOLNSGRQSPSQNERWARPKHILEDEL
Db	1021	LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQ
à i	90	EQROSRNQSTTYPVYTESTDXGLKROPHFGQQECVSPYRSRGANGSETNRVGSNHGINO 1123
<u>8</u> 8	1081	KÖSKNÖSTITYYVIESTUUKHEKFÜPHEGÜĞE VSFIRSKGANGSEINN VOSMISLAN TIT. SOSLOOBDDYBDDKPTNYSERYSEEBQHEEBERPTNYSIKYNEEKRHUDQPIDYSLKY 118:
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ζ	1184	4
QQ	1201	IPSSQKQSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRONQLHPSSAQSRSGQP 126
. QZ	1244	QKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQ 1303
ò		IKGKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPSGAKS
QQ	1321	
δλ	1364	GAQTPKSPPE
qq	1381	JIPKSFPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDL 144
ģ	1424	PPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLP 148:
Ωp	1441	SPGÓTMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLP 150
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ò	1724	ECINSAMPKGKSHKPPRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKP
qq	1741	CINSAMPKGKSHKPFRVKKIMDQVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNT 180
ò	1784	RTRVRXNADSKONLNAERVFSDNKDSKKONLKONSKDFNDKLFNNEDRVRGSFAFDSP 184:
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                   Familial adenomatous polyposis coli; APC; tumour suppressor; therapy; chromosome 5q21; tumourigenesis; retinoblastoma; colorectal tumour; FAP; Gardner's Syndrome; GS; predisposition.
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Pred. No. 0;
2; Mismatches
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Anand R,
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Best Local Similarity 99.8%;
Matches 2836; Conservative
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UNIV UTAH.
ZENECA PHARM.
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, Groden J,
B, Hedge PJ;
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N-PSDB; AAV56447.
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Thliveris A, Gr
Vogelstein B, F
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16-JAN-1991;
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                                    SHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSR
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241	EAERSSQNKHETGSHDAERQNEGGGVGEINMATSGNGQGSTTRMDHETASVLSSSSTHSA 300	,	
301	PRRLTSHLGTKVEMVYSLLSMLGTHDXDDMSRTLLAMSSSODSCISMROSGCLPLLI	ò	1381
301	PRELITERIOTIVE WAYS LEGINICATED TO DESCRIPTION 36	qq	1381
361	HGNDKDSVIJGNSRGSKEBBBBBBBBBHHNIIHSODDDKRGEBEIBVIHIIBOZVGEG 42	δ	1441
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481	CRYGLTUDHYG TTERRYAGWALTUNTEGDYANKATICSKKGCWALVACKEEEDL 54	QC	1561
. 44	OOVTASVI RNI SWRADIVNSKKTI BRVGSVKAI MECAI BVKKESTI KSVI SAHCT 60	Š	1621
541	QQVIASVIRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT 60	qq	1621
601	ENKADICAVDGALAFLVGTLTYRSOTNTLAITESGAGILRNVSSLJATNEDHROTLFRVN 66	ò	1681
601	ENXADICAVDGALAFLVGTLITYRSÇINTLAIIESGGGGILRNVSSLIATNEDHROILRENN 66	đ	1681
661	CLOTLLOHLKSHSLTIVSNACGTLWNLSARNPKDOBALWDMGAVSMLKNLIHS	ò	1741
661	CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQRALWDMGAVSMLKNLIHSKHKMIAM 72	qq	1741
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This sequence represents a human familial adenomatous polyposis coli (APC) protein isolated from 87 cDNA clones. The gene for the protein is present on human chromosome 5Q21 and is also referred to as adenomatous polyposis coli gene. It is a tumour suppressor gene, and mutations in colorectal tumours, and especially familial adenomatous polyposis (FAP) and Gardner's Syndrome (GS). The protein can be used in therapy to replace lack of native functional protein can be used in therapy to used for gene therapy. The mucleic acids that encode them can also be used as probes and primers in detection of the cancers and predisposition to it. (Updated on 25-MAR-2003 to correct PR field.)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDWGAVSMLKNLIHSKHKMIAM 720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               421 WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQ
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                                                                                                                                                                                                                                               99.7%; Score 14533; DB 2; Length 2843;
llarity 99.8%; Pred. No. 0;
Conservative 2; Mismatches 5; Indels 0;
      Disclosure, Col 63-78; 102pp; English.
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Best Local Similarity
Matches 2836; Conserv
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SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Adenomatous polyposis coli protein - useful in the treatment of cancers associated with mutation(s) on human chromosome 5q21.
                    SPESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEVNDG
                                                                            2581 SEKAKSEDEKHVNSISGTKOSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
                                                                                                                                                                                                    QAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERT
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                                                            RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES
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                                                                                                                     SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
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Albertsen
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Nakamura Y,
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Anand R,
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A, Groden J, A
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Vogelstein B, I
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12-AUG-1994;
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1861 SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR 1920 1921 GQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNPAIENTPVCFSHNSSLSSLSDIDQENN 1980	SKULPUKGAAIDEKLÜNKALENTPVCFSHNSSESSLSDIUG GEBSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD 	QY 2041 ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDLKDLKDSEHGLSPDSENFD 2100	2101 WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT 216 2101 WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT 216	2161 SNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGGMKQPLQAN 222º [Qy 2221 MPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSFSEGQTATISPRGAKPSVKS 2280 [Oy 2281 ELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIGSPGRNSISPGRNGISPPN 2340	Qy 2341 KLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQNLTKQTGLSKNASSIPRSESASKG 2400 2341 KLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQNLTKQTGLSKNASSIPRSESASKG 2400	nnngngankkvelsrmsstkssgsesdrserpvlvrqstfikeadsptlrrkleesa 246. 	SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLS 	2521 RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES 258	581 SEKAKSEDEGTVNSISGTKOSKENOVSAKGTWRKIKENEFSPTNSTSOTVSSGATNGAES 264 [2641 KTLIYQNAPAVSKTEDVWVRIEDCPINNRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN 270	QAKQNYGNGSYPMRTYGLENRLISSIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERT 276 [Qy 2761 PFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSKT 2820 [Oy 2821 DSTESSGTQSPRHSGSYLVTSV 2843 Db 2821 DSTESSGTQSPRHSGSYLVTSV 2843	RESULT 8 AAB23011 ID AAB23011 standard, protein, 2843 AA.	AX AAB23011; XX XX
	841 LDSSRSEKDESTERERGIGLGNYHPATENPGTSSKRGLGISTTAAQIAKVMEEVSAIHTS 900 901 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRS 960	NDSLNSVSSNDGYRGGWRPSIESYSEDDESKTGSYGOYPADLAHKIHSANHMDNDGE 10 NDSLNSVSSNDGYRGGWRPSIESYSEDDESKTGSYGOYPADLAHKIHSANHMDNDGE 10 NDSLNSVSSSDGYGRGGWRPSIESYSEDDESKTGSYGOYPADLAHKIHSANHMDNNGE 10	DDTPINYSLKYSDEQLNSGROSPSONERWARPKHIIEDEIKOSGROSTTYPVYTE 108	1081 STDDKHLKRQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDXEDDKP 1140 	IPSSQKQSFSFSKS 1	SSGQSSKTEHWSSSSENTSTPSSNAKRONOLHPSSAOSRSGOPQKAATCKVSSINOBTIQ 126	TYCVEDTPICFSRCSSLSSLSSABBIGCNOTTORADSANTLOIAETKGKIGTRSAEDPV 132 TYCVEDTPICFSRCSSLSSLSSABBIGCNOTTORADSANTLOIAETKGKIGTRSAEDPV 132 TYCVEDTPICFSRCSSLSSLSSAEDETGCNOTTORADSANTLOIAETKRKTGTRSAEDPV 132	SEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFPGGAKSPSKSGAQTPKSPPEHYVQET 138	PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTWPPSRSKTPP 14	41 PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGF 150	1501 SCSSLSALSLDEPFIQXDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1560 	KDLLDDSDDDDIELLEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPS 16	ONFLOPOKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 16	SGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP 17	PRVKKIMDOVQQASASSSAPNKNQLDGKKKKPTSPVKP1PQNTEYRTRVRKNADSKONLN 18 	1801 AERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND 1860 	1861 SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQSANKTQAIAKQPINR 1920

06:02:19 2004

Thu Aug 26

Query Match

99.7%; Score 14533; DB 3; Length 2843;

1021 LDTPINYSLKYSDBQLNSGRQSPSQNBRWARPKHIIBDBIKQSBQRQSRNGSTTYPVYTE 1080

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Sequence 2843 AA
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APC gene; Adenomatous Polyposis Coli gene; human; chromosome 5q21; familial adenomatous polyposis; FAP locus; Gardner's syndrome; GS; sporadic tumour; adenoma; carcinoma; cancer; lung; breast; colon; rectum; bladder; liver; sarcoma; stomach; prostate; leukaemia; lymphoma; tumour suppressor; anti-APC antibody; detection; diagnosis; prognosis; genetic predisposition; drug screening; DP2.5; splice variant.
                                                                                                                                                                                                                                                                                                                                                                            Detecting Adenomatous Polypopsis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies t specifically bind to APC protein and detecting the complex formed.
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Thliveris A, Nakamura Y, Vogelstein B;
                   Human APC protein (splice variant 1).
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91GB-00000963.
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The invention relates to a novel method for detecting Adenomatous polyposis Coli (APC) protein in a sample. The method involves contacting the sample with antibodies which specifically binds to the 2813 amino acid form of the human APC protein, or to a mutant APC protein, and detecting an APC-antibody complex. Mutations in the APC gene play a role in tumorigenesis, indicating that it is a tumour suppressor gene. It is cocated on chromosome 521, which corresponds to the FAP (familial adenomatous polyposis) locus. FAP is an autosomal dominant inherited disease in which affected individuals develop hundreds to thousands of adenomatous polypes in the colon and rectum, some of which progress to malignancy. The FAP locus is often found to be deleted in sportatio (i.e., non-familia) adenomas and carcinomas, and chromosome 5q deletions have also been observed in tumours of the lung, breast, colon, rectum, non-familia) adenomas and carcinomas, and chromosome 5q deletions have also been observed in tumours of the lung, breast, colon, rectum, lung been observed in tumours of the lung, breast, onlon, rectum, labo been observed in tumours of the lung, breast, colon, rectum, labo been observed in tumours of the lung, breast, colon, rectum, labo been observed in the development of the plant mutations in the APC gene play a ker, TBI, TB2, and MCC, it is thought that mutations in the APC gene play useful for detecting APC protein and its mutati forms in foeral tissue, placental tissue, aminotic fluid, blood, serum or a tumour sample. The method is useful for diagnositing or prognosing neoplastic tissue, for detecting a genetic predisposition to cancer, for detecting germine a genetic predisposition to cancer, for detecting germine a genetic predisposition to cancer, for detecting germine a genetic predisposition to cancer, for detecting germine and spiles variant of the human APC protein.

This variant is more abundant than the 2742 amino acid variant (AAB23012)

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                                                                                                                                                 The invention describes a transgenic Drosophila whose genome comprises the full-length human colon cancer gene Adenomatous Polyposis Coli (APC) allowing regulated mis-expression of the APC gene resulting in developmental abnormalities. The transgenic files are used to screen and validate efficacy of anticancer drugs, to identify new target proceins interacting with beta-catenin, genes which interact with human APC, to study the biochemical function of human APC and to identify additional components of the Drosophila Wat/Wg signalling pathway. In particular the files are used to screen potential drugs against colon cancer. This is the amino acid sequence of the human adenomatous polyposis coli (APC) protein DNA encoding which is incorporated in the transgenic files
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                                                                               New transgenic Drosophila containing the human colon cancer gene Adenomatous Polyposis Coli is useful as an assay model to screen for drugs, particularly against colon cancer.
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This sequence represents a human APC protein which is used in a method of identifying candidate drugs for use in familial adenomatous polyposis (TAPP) patients, or patients with increased risk of developing cancer. The protein can also be used to determine the presence or absence in a cell of wild type adenomatous polyposis coli (APC) gene or a downstream or protein in the APC transcription regulatory pathway. This method involves introducing a TCF-responsive reporter gene into the cell, and measuring transcription of the reporter gene where a cell which supports active downstream protein of the APC transcription regulatory pathway. The protein can also be used in a method of diagnosing cancer in a sample cancer or other cancer associated with TAPP, comprising the beta-catenin binding site
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2; Mismatches
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DSTESSGTQSPKRHSGSYLVTSV
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Best Local Similarity 99.8%;
Matches 2836; Conservative 2
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121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180

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Disclosure; Page 74-81; 83pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Human, Tcf-4 protein; transcriptional activation factor; beta-catenin; apoptosis; colorectal cancer; Familial Adenomatous Polyposis; FAP; APC; adenomatous polyposis coli; recombinant adenovirus; Ad-Mini-Me; therapy; GFP; green fluorescent protein; GFP/CAPC fusion protein; cytostatic.
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                                                                                             SFESISPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG
                                                                                                                               RPAKRHDIARSHSESPSKLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES
                                                                                                                                                                     SEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
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         KLSQLPRISSPSTASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKG
                   RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES
                                                                                                                                                      SEKAKSEDEKHVNSISGTKOSKENOVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES
                                                     LNOMMNGNGANKKVELSRMSSTKSSGSESDRSERPVLVROSTFIKEAPSPTLRRKLEESA
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Vogelstein B, He T;
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The present sequence is a transcriptional activation protein related to the invention. The invention relates to human Tcf4 by proteins and their corresponding cDNA molecules which encodes transcriptional activation activation in colorectal peithelial cells. Moreover it has been found that adenomatous polyposis coli (APC) regulates this transcription in colorectal peithelial cells. Moreover it has been found that adenominated peithelial cells. Moreover it has also provides a recombinant adenovimus, Ad-Mini-Me ie., ApC Minus its also provides a recombinant adenovimus, Ad-Mini-Me ie., ApC Minus its almino- and carboxyl -terminal Ends which expresses a fusion protein, creen fluorescent protein (GFP)/CAPC containing GPP fused to the central chinch appoptosis or treating colorectal cancer. These fusion proteins are useful for treating cancer. e.g. colorectal cancer, and other cancers are useful for treating cancer. Howan Tcf-4 cDNA provides an increased risk of developing cancer. Human Tcf-4 cDNA provides and excellent system for screening agents for their ability to promote callery. Human regration in cells or in an animal. It also provides metals cancer in a sample suspected of being neoplastic
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Best Local Similarity 99.8
Matches 2836; Conservative
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Human Tcf-4B protein; transcription factor; beta-catenin;
Adenomatous polyposis coli; APC; transcriptional activation;
Tcf responsive reporter gene; APC transcription regulatory pathway;
familial adenomatous polyposis; PAP; cancer; colorectal; thyroid; brain;
medulloblastoma; breast; head; neck; desmoid tumour; osteoma; cytostatic.
                                                                                                                                                                                                                                                                                                                                         Determining wild-type adenomatous polyposis coli protein for diagnosing cancer comprises introducing a Tcf responsive reporter gene having upstream sequences of c-MYC into a cell.
                                                                         Protein used in cancer diagnosis associated with APC/beta-catenin
                                                                                                                                                                                                                                                                           (UYJO ) UNIV JOHNS HOPKINS SCHOOL MEDICINE.
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         AAY70304 standard; protein; 2973
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The present sequence is a protein involved in cancer diagnosis associated with APC or beta-catenin mutations. Human Tcf-4B protein expressed in colorectal epithelium transactivates transcription when associated with beta-catenin. Adenomatous polyposis coli (APC) regulates this transcriptional activation, alleast in part by binding to beta-catenin. Determining wild-type APC protein for diagnosing cancer comprises introducing a Tcf responsive reporter gene having upstream sequences of any into a cell and measuring transcription of the reporter gene. The candidate drug identified is useful for treating familial adenomatous polyposis patients with APC or beta-catenin mutations and patients with medulloblastoma, desmoid tumour, osteoma, breast, head and neck brain, 9 9 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM .; 0 Length 2973; Indels . 9 DB 3; 2; Mismatches Score 14526; Pred. No. 0; 99.7%; Query Match
Best Local Similarity 99.7
Matches 2835; Conservative Sequence 2973 AA;

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> 120 120 180 RGFVNGSRESTGYLEELEKERSLLLADLDKEKEKOWYYAQLQNLTKRIDSLPLTENFSL 180 QIDLIRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240 ASSGOIDLIERLKEINLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLONLTKRIDSLPLTENFSL ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 61 121 61 121 181 P g 8 g δ ઠે

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	ARESULT 13 ARES6634 ID AARS6634 standard; protein; 2843 AA. XX AARS6634 E-MAR-2003 (irevised) DT 21-UNN-1995 (first entry) XX Adenomatous polyposis coli protein (APC). XX Adenomatous polyposis coli protein gene; familial adenomatous polyposis; XX XX XX XX XX XX XX XX XX XX XX XX XX
1261 TYCVEDTPICFSRCSSLSSASDEIGCNOTTQEADSANTLQIABIKEKIGTRSAEDPV 1320 1321 SEVPAVSQHPRTKSSRLQGSSLSSBARHKAVEPSGAKSPSKSGAQTPKSPPEHTVQFT 1380 1321 SEVPAVSQHPRTKSSRLQGSSLSSBARHKAVEPSGAKSPSKSGAQTPKSPPEHTVQFT 1380 1321 SEVPAVSQHPRTKSSRLQGSSLSSBARHKAVEPSGAKSPSKSGAQTPKSPPEHTVQFT 1380 1381 PLAFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP 1440 1441 PPPQTAGTKREVPKNKAPTAEKRESGEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP 1440 1441 PPPQTAGTKREVPKNKAPTAEKRESGEPCSGMVSGIISPSDLPDSPGGTMPPSRSKTPP 1440 1441 PPPQTAGTKREVPKNKAPTAEKRESGEPCSGMVSGIISPSDLPDSPGGTMPPSRSKTPP 1440 1501 SCSSLSALSLDBPPIQKOVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1560 1501 SCSSLSALSLDBPPIQKOVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDSE 1560 1501 SCSSLSALSLDBPPIQKOVELRIMPPVGENDNGNETESEQPKESNENQEKARAKTIDSE 1560 1501 GCSSSLSALSLDBPPIQKOVELRIMPPVGENDNGNETESEQPKESNENQEKARAKTIDSE 1560 1501 GCSSSLSALSLDBPPIQKOVELRIMPPVGENDNGNETESEQPKESNENGEKARAKTIDSE 1560 1501 GNSLLDDSDDDIBILEBCIISAMPTKSSRKKKRARPAGNAKLPPVARKEGGLPVYKLLDS 1620 1501 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680 1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680 1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680 1621 GNRLQPQKHVSFTPGGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680 1621 GNRLQPQKHVSFTPGGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680 1621 GNRLQPQKHVSFTPGGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1680 1621 GNRLQPQKHVSFTPGGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGKSHKP 1740 1681 SGEFEKRDTIPTEGRSTDEAQGKTSSVTIPELDDNKAEEGDILAACTNSAMPKGKSHKP 1740 1741 FRVKKINDQVQQASASSABNKNQLDGKKKPTSPVKPIPQNTBYRTRYRKNADDSKNNLN 1800 1741 FRVKKINDQVQQASASSABNKNQLDGKKKPTSPVKRPIPQNTBYRTRYRKNADDSKNNLN 1800	1801 AERVFSDNKDSKKQNLKANSKDPNDKLPNNEDRYRGSFAFDSPHHYTPIEGTPYCFSRND 1860 1801 AERVFSDNKDSKKQNLKANSKDPNDKLPNNEDRYGSFAFDSPHHYTPIEGTPYCFSRND 1860 1801 AERVFSDNKDSKKQNLKANSKDPNDKLPNNEDRYGSFAFDSPHYTPIEGTPYCFSRND 1860 1801 SLSSLDPDDDDVDLSREKAELRKAKENKESEAKYTSHTELTSNQGSANKTQALAKQPINR 1920 1812 SLSSLDPDDDVDLSREKAELRKAKENKESEAKYTSHTELTSNQGSANKTQALAKQPINR 1920 1921 GQPKPILQKQSTPPGSSKDIPDRGAATDEKLQNFATENTPYCFSRNSSLSSLSDDDDRN 1980 1981 NKENEPIKETEPPDSQGPESKPQASGVAPKSFHVEDTPYCFSRNSSLSSLSDDDDRN 1980 1981 NKENEPIKETEPPDSQGPESKPQASGVAPKSFHVEDTPYCFSRNSSLSSLSDDDDRN 1980 1981 NKENEPIKETEPPDSQGPESKPQASGVAPKSFHVEDTPYCFSRNSSLSSLSIDDDDRN 1980 2041 ECISSAMPKKKPSRLKGDREKKSPRNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPRNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPRNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPRNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPRNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPRNAGGLIGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPRNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPRNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPNAGGLIGEDLTLDLKDIQPRDSEHGLSPDSENFD 2100 2041 ECISSAMPKKKPSRLKGDNEKKSPNAGGLIGEDLTLDLKDIQRPDRGKCPPT 2160 2041 ECISSAMPKKKPSRLKGDNEKKSPNAGGLIGEDLTLDLKDIQRPDRGKCPPT 2160 2041 ECISSAMPKKKPSRLKGDNEKKSPNAGGLIGEDLTLDLKDIQRPDRGKCPPT 2160 2041 ECISSAMPKKKPSRLKGDNEKKSPNAGGLIGEDLTLDLKDIQRPDRGKCPPT 2160 2041 ECISSAMPKKKPSRLKGDNEKKSPNAGGLIGEDLTLDLKDIQRPDRGKPPT 2160 2161 IN WKAIQEGANSITVSSLGAAAACLSRQSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSSS

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Best Local Similarity 99.6%; Pred. No. 0;
Matches 2833; Conservative 6; Mismatches AA; Sequence 2843 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6 B 6

FRVKKIMDOVQQASASSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLN KOLLDDSDDDDIBILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKDSQLPVYKLLPS AERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRND NDSLNSVSSNDGYGKRGQMKPSIESYSEDDESKFCSYQQYPADLAHKIHSANHMDDNDGE LDTPINYSLKYSDEQLNSGROSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE STDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 상 원 6 6 6 6 6 6

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       ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD
                                           WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT
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Anand R, Nakamura Y, Groden J, Kinzle: , Vogelstein B, Albertsen H, White RL;

Hedge PJ, Ar Carlson M,

91GB-00000963. 91GB-00000974. 91GB-00000975.

91US-00741940. 91GB-00000962

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                                                                                                                                                                 AAQ72297 is a cDNA isolated from the human adenomatous polyposis coli (APC) gene, it encodes the tumour repressors described in AAR63507 and AAR63508. Determination of alterations in APC or its expression products, can be used for the diagnosis and prognosis of cancer e.g. colorectal, lung and breast tumours; and for determining predisposistion to certain cancers such as familial adenomatous polyposis (FAP) and Gardner's syndrome. The wild type APC gene (or a part of it) can be used therapeutically to restore gene function, while primers and probes derived from the cDNA (AAQ72313-400 and AAQ72541-569) can be used to detect mutations. Also APC proteins or analogues can be administered to compensate for a defective gene, and epithelial cells, of transgenic animals carrying a mutated APC allele are useful for detecting therapeutic agents able to suppress tumorigenesis. (Updated on 25-MAR-2003 to correct PA field.)
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New human adenomatous polyposis coli DNA encoding tumour repressor - derived primers and probes for diagnosis, prognosis and treatment of
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Adenomatous polyposis coli; tumour repressor; Gardner's syndrome; familial adenomatous polyposis; cancer diagnosis and prognosis; tumorigenesis suppression.

Adenomatous polyposis coli tumour repressor.

(revised) (first entry)

25-MAR-2003 23-MAY-1995

AAR63508

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AAR63508 standard; protein; 2842

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detecting somatic alteration of wild-type adenomatous polyposis coli) protein in a tumour tissue isolated from a human (the alteration indicating neoplasta of the tissue). The method of the invention is useful in diagnosis or prognosis of a neoplastic tissue of a human the method is useful in detection of genetic predisposition to cancer. The present sequence represents a peptide sequence used in the method of the
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                                                                                                                                        KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN
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                                           RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRTGSSSSILSASSES
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, Thliveris A, Vogelstein B;
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OY 2761 PFSSSSSKHSSPSGTVAARVTPFNVNPSPRKSSADSTSARPSOIPTPVNNVTKKRDSKT 28 Db 2761 PFSSSSSKHSSPSGTVAARVTPFNVNPSPRKSSADSTSARPSOIPTPVNNNTKKRDSKT 28 OY 2821 DSTESSGTOSPKRHSGSYLVTSV 2843 Db 2821 DSTESSGTOSPKRHSGSYLVTSV 2843 Db 2821 DSTESSGTOSPKRHSGSYLVTSV 2843	RESULT 10 US-08-821-355A-7 ; Sequence 7, Application US/08821355A ; Patent No. 5851775 ; GENERAL INPORMATION:	APPLICANT: APPLICANT: APPLICANT: APPLICANT:	# APPLICANT: Kinzler, Kenneth # APPLICANT: Vogelstein, Bert # APPLICANT: Sparks, Andrew # TITLE OF INVENTION: Beta Catenin, TCF-4, and APC # TITLE OF INVENTION: Beta Catenin, TCF-4, and APC	NUMBER OF SEQUENCES: 11 CORRESPONDENCE ADDRESS: ADDRESSES: ADDRESSES MITCOFF, Ltd.		COMPUTER READABLE FOI MEDIUM TYPE: Disk COMPUTER: IBM COM	OPENATURE SIZERM: DOS SOFTWARE: FeatSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: PAPLICATION NUMBER: US/08/821,355A	FILING DATE: CLASSIFICATION PRIOR APPLICATION IN	AFIGNEY CARE: AFIGNEY CARE: NAME: Kagan, Sarah A REGISTRATION NUMBER: 32,145	TELECONTUNICATION INFORM TELECONTUNICATION INFORM TELEPHONE: 202-508-929 TELEFAX: 202-508-929		STRANDEDNESS: TOPOLOGY: li MOLECULE TYPE:	Query Match Query Match Best Local Similarity 99.8%; Score 14533; DB 2; Length 2973; Best Local Similarity 99.8%; Pred, No. 0; Matches 2836; Conservative 2, Mismatches 5, Indals 0. Gans	LKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 6 LKQVFALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 6 LKQVFALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKOLQGSIEDEAM 6 LKQVFALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKOLQGSIEDEAM 6	61 ASSQ1DLLERLKELNLDSSNPPGVKLRSKMSLRSYGSKBGCSPVPMGSFPR	

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         PKASHRSKQRHKQSLYGDYVFDINRHDDNRSDNFNTGNMTVLSPYLNITVLPSSSSSRGS
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NAME: Kagan, Sarah A
REGISTRATION NUMBER: 32,145
REFERENCE/DOCKET NUMBER: 1107.05064
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-508-9100
TELEFAX: 202-508-9100
TELEFAX: 202-508-9299
TELEFAX: 202-508-9299
TELEX: 97430 BMB UT
SEQUENCE CHARACTERISTICS:
LENGTH: 2973 amino acids
                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: No. 5998600e
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Best Local Similarity 99.8%;
Matches 2836; Conservative 2
       NAME: Kage
REGISTRATIC
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Query Match
Best Local Similarity 99.8%;
Matches 2836; Conservative
                                                                                                                                                    LENGTH: 2973
TYPE: PRT
ORGANISM: Homo sapiens
US-09-136-605-7
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RESULT 12
US-09-136-605-7
Sequence 7, Application US/09136605A; Patent No. 6140052; GENERAL INFORMATION:
APPLICANT: He, Tong-Chuan

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APPLICANT: Kinzler, Kenneth
APPLICANT: Vogelstein, Bert
TITLE OF INVENTION: Bert Catenin, TCF-4, and APC Interact to
TITLE OF INVENTION: Prevent Cancer
FILE REFERENCE: 1107.75741
CURRENT APPLICATION NUMBER: US/09/136,605A
CURRENT APPLICATION NUMBER: 08/821,355
EARLIER FILING DATE: 1998-08-20
EARLIER PILING DATE: 1999-03.0
EARLIER PILING DATE: 1998-01-06
NUMBER OF SEQ ID NOS: 28
NUMBER OF SEQ ID NOS: 28
SOFTWARE: FREESEQ for Windows Version 3.0
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1 GSAAALRNLMANRPAKYKDANIMSPGSSLPSLHVRKQKALBAELDAQHLSETFDNIDNLS 78 1 PKASHRSKQRHKQSLYGDYVPDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGS 84	LDSSRSEKDRACHARDEN GELVFDLINNEDDRINSDRFILGEN TERFLEN LIVERSSSSRGS 9** LDSSRSEKDER SLERERGIGLGNYHPATEN PGTSSKRGLQISTTAAQIAKVMEEVSALHTS 90	DSSKSEKORDLEKERGIGLGGNYHPATENPGISSKRGLQISTTAAQIAKVMEEVSALHT EDRSSGSTTELHCVTDERNALRRSSAAHTHSNYTVHTKSENSNRTCSMPYAKLEYKRS BDRSSGSTTELHCVTDERNALRRSSAAHTHSNYYNFYKSENSNRTCSMPYAKLEYKRS	NDSLNSVSSNDGYGKRG@MKPSIESXSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE 10	21 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHILEDEIKQSEQRQSRQSTYPVYTE 108 21 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHILEDEIKQSEQRQSRQSTYPVYTE 108 21 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHILEDEIKQSEQRQSRQSTYPVYTE 108	STDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP 114	41 INVSERYSEEBQHEEEERPTNYSIKXNEEKRHVDQPIDYSLKYATDIPSSCKOSFSKS 1	SSGOSSKTEHMSSSSENTSTPSSNAKRONOLHPSSAOSRGOPOKAATCKVSSINOETIO 12	51 TYCVEDTPICFSRCSSIASTEDSIGNOTTOEADSANTLOIABIKGKIGTRSAEDPV 132	21 SEVPANSOHPRIKSSKLOGSSLOGESTREAKAVEFPSGAKSPSKSGAOTRKSPFHYVOET 138 21 SEVPANSOHPRIKSSKLOGSSLSSRRKAVEFPSGAKSPSKSGAOTRKSPFHYVOET 138 21 SEVPANSOHPRIKSSRLOGSSLSSPSKRAVERSKARSKSGAOTRKSPFHYVOET 138	1 PLMFSRCTSVSSLDSFESRSIASSVOSEPCSGWVSGTISPSDLDSFGCTWFFSRSTTPP 144	PPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHTATESTPDGF 150	1 SCSSSLSALSLDEPFIQKOVELRIMPPVQENDNNNHTESSOPKESNENDEKTIDSE 156 1 SCSSSLSALSLDEPFIQKOVELRIMPPVQENDNNNHTESSOPKESNENDEKTIDSE 156 1 SCSSSLSALSLDEPFIQKOVELRIMPPVQENDNNNHTESSOPKESNENDEKTABKTIDSE 156	XDLLDDSDDDDIBILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPS 162 	621 QNRLOPOKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 168	SCEFEKEDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKP 17	KIMDQVQQASASSSAPNKNQI 	1801 AERVFSDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSEND 1860 	

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240 BAERSSQNKHETGSHDAERQNEGQGVGEINMAISGNGQGSTTRMDHETASVLSSSSTHSA
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                                                      PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL
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                                                                       APPLICANT: ANAMA, RAKESH
APPLICANT: CARLSON, MARY
APPLICANT: GARLSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: HEDGE, PHILIP J.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKHAMURA, YUSUKE
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APPLICANT: NAKHAMURA, YUSUKE
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APPLICANT: NAKHAMIRA
APPLICANT: NAKHAMURA, YUSUKE
APPLICANT: NAKHAMURA, YUSUKE
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COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPUTER: IBM PC Compatible
COMPATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/741,940
FILING DATE: 19920109
CLASSIFICATION: 435
ATTONNEY/AGENT INPORMATION:
NAME: REGISTRATION NUMBER: 32.141
REFERENCE/DOCKET NUMBER: 31.141
REFERENCE/DOCKET NUMBER: 1107.035574
TELEFRANCE 202-508-9100
TELEFRANCE 202-508-9100
TELEFRANCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                      STREET: 1001 G Street, NW CITY: Washington STATE: D.C.
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Pred. No. 0;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 99.7%;
Matches 2835; Conservative
                                                         ALBERTSEN, HANS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
STRANDENNESS: single
TOPOLOGY; linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 20001-4598
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IMMEDIATE SOURCE:
CLONE: APC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-07-741-940-7
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OY 2461 SPESLSPESRPASPTRSQACTPVLSPSLPDMSLSTHSSVQACGWRKLPPNLSPTIETNDG 2520 2460 SFESLSPSSRPASPTRSQACTPVLSPSLPDMSLSTHSSVQACGWRKLPPNLSPTIETNDG 2519 04 2521 RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSLPRVSTWRRTGSSSSILSASSES 2579 2520 RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES 2579 05 2581 SEKAKEDEKHYNSISGTROSGTWKREHSKHSSBLPRVSTWRTGSSSSILSASSES 2579 06 2580 SEKAKEDEKHYNSISGTROSKENOVSAKGTWRKIKENEFSPTNSTGGTVSSGATNGABS 2640 07 2641 KTLIYQWAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSGATNGABS 2659 09 2640 KTLIYQWAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSGATNGABS 2659 09 2701 QAKQNVGNGSVPRTVGLENRLTSFIQVDAPDQXGTEIKPGQNNPVPVSETNESSIVERT 2760 09 2700 QAKQNVGNGSVPRTVGLENRLTSFIQVDAPDQXGTEIKPGQNNPVPVSETNESSIVERT 2760 09 2761 PPSSSSSSKHSSPSGTVAARVTPPNYNDSPRKSSADSTSARPSQIPTPVNNNTKKRDSKT 2819 09 2761 PFSSSSSSKHSSPSGTVAARVTPPNYNDSPRKSSADSTSARPSQIPTPVNNNTKKRDSKT 2819 09 2821 DSTBSSGTVSARRYGSPNATVTPPNYNDSPRKSSADSTSARPSQIPTPVNNNTKKRDSKT 2819 09 2820 DSTBSSSGTVSARRYGGSVLVTSV 2842	US-08-29-468-7 Sequence 7. Application US/08289548A Patent No. 5492120. GENERAL INFORMATION: APPLICANT: ALBERTSEN, HANS APPLICANT: CARLSON, WARY APPLICANT: CARLSON, WARY APPLICANT: HEOGE, PHILIP J. APPLICANT: HEOGE, PHILIP J. APPLICANT: HEOGE, PHILIP J. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. APPLICANT: MARKHAM, ALEXANDER F. ALEXALITANDERSEN: 100 G SECERT, MW CONDITES: LO. COUNTRY: Washington STATE: D.C. CONDITY: Washington STATE: D.C. CONDITY: Washington STATE: D.C. CONDITY: MARKHAM: ALEXANDER F. DOG MARKHAM MARE: Magning TYPE: PLOYER FLOOR AND ALEXANDER CONDITES: TALLONDERSEN: 1107,46943 FILING DATE: 12-406-1904 MARE: Magning STATER: 1107,101-163 MATCHANDER MARKER: 1107,46943 FILING DATE: 202-508-100 TELEFORMICATION: APR STATER MARKHAM: 202-508-100 TELEFORM: ALEXALTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS:
1381 PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP 1440 1380 PLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPP 1439 1441 PPPQTAQTKEEVPKNKAPTAEKRESGPKQAVNAAVQRVQLPDADTLLHFATESTPDGF 1500 1440 PPPQTAQTKEEVPKNKAPTAEKRESGPKQAAVNAAVQRVQLPDADTLLHFATESTPDGF 1500 1441 PPPQTAQTKEEVPKNKAPTAEKRESGPKQAAVNAAVQRVQLPDADTLLHFATESTPDGF 1500 1501 SCSSSLSALSLDEPFTQKDVELRIMPPVQENDNGNFTESEQPKESNENQEKBAEKTIDSE 1560 1501 SCSSSLSALSLDEPFTQKDVELRIMPPVQENDNGNFTESEQPKESNENQEKBAEKTIDSE 1560 1501 SCSSSLSALSLDEPFTQKDVELRIMPPVQENDNGNFTESEQPKESNENQEKBAEKTIDSE 1560 1560 KDLLDDSDDDDIEILEECIISAMPTKSSRKGKKPAQTASKLPPPVARKPSQLPVYKLLPS 1619 1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1679 1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1679 1621 QNRLQPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQ 1679 1681 SGEFEKRDIIPFGGRSTDEAQGGKTSSVTIPELDDNKAEGGDLIAECINSAMPKGKSHKP 1740 1680 SGEFEKRDTIPFTGGRSTDEAQGGKTSSVTIPELDDNKAEGGDLIAECINSAMPKGKSHKP 1739 1741 FRVKKIMDQVQQASASSSAPNRQQLDGKKKKRPTSPVKPIPQNTEYRTRVKKNADSKNNLN 1800 1741 FRVKKIMDQVQQASASSSAPNRQQLDGKKKKRPTSPVKPIPQNTEYRTRVKNADSKNNLN 1799	AERVFSDNKDSKKQNLKANSKOPRDKLENNEDRVRGSPAFDSPHHYTPIEGTPYCFSRND 186 AERVFSDNKDSKKQNLKANSKOPRDKLENNEDRVRGSPAFDSPHHYTPIEGTPYCFSRND 185 SLSSLDFDDDDVDLSREKAELRKAKENBERANTSHTELTSNQSANKTQALAKQPINR 192 SLSSLDFDDDDVDLSREKAELRKAKENBERANTSHTELTSNQSANKTQALAKQPINR 193 SLSSLDFDDDDVDLSREKAELRKAKENBERANTSHTELTSNQSANKTQALAKQPINR 191 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 198 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GQPKPILQKQSTPPQSSKDIPDRGAATDEKLQNPAIENTPVCFSRNSSLSSLSDIDQENN 199 GCSSAMPKKKRPSRLKGDNBXHSPRNMGGILGEDLTLDLKDIGRPPSEHGLSPDSENPD 210 ECISSAMPKKKRPSRLKGDNBXHSPRNMGGILGEDLTLDLKDIGRPPSEHGLSPDSENPD 210 ECISSAMPKKKRPSRLKGDNBXHSPRNMGGILGEDLTLDLKDIGRPPSHTIPPQEEKPPT 215 WKALQEGANSIVSSLSTRSTRSGSSDSDILGHANSTSPRGAYRSPRGAYFSYNGS 227 HILLINGHANGANGANASSSSTSPVSKKGPPLKTPAASKSPEBGGGTATTSPRGAKPSVKS 228 HILLINGHANGANKVPLSRRSGSRDSTPSRPAQQPLSRPICKGTSRNSSIPRSESASKG 240 LLINGHANGANKKVPLSRRSGSSDSSTPSRPAQQPLSRPICKGTGLSVASSIPRSESASKG 240 LLINGHANGANKKVPLSRPSTKSSGSSBSBRSRRPVLVRQCGLSVANSSIPRSESASKG 240 LLNGMANGGANKKVPLSRPSTKSSGSSBSBRSRRPVLVRQCSTPIKKATSSPGTLRRKLEESA 245 LLNGMANGGANKKVPLSRPSTKSSGSSBSBRSRRPVLVRQCSTPIKKATSSPGTLRRKLEESA 245 LLNGMANGGANKKVPLSRPSTKSSGSSBSBRSRRPVLVRQCSTPIKKATSSPGTLRRKLEESA 245 LLNGMANGGANKKVPLSRPSTKSSGSSBSBRSRRPVLVRQCSTPIKKATSSPGTLRRKTEESA 245 LLNGMANGGANKKVPLSRPSTKSSGSSBSBRSRRPVLVRQCSTPIKKATSSPGTLRRKTEESA 245 LLNGMANGGANKKVPLSRPSTKSSGSSBSBRSRRPVLVRQCSTPIKKATSSPGTLRRKTEESA 245 LLNGMANGANKKVPLISRPSTKSSGSSBSRSRRRPVRQCSTPIKKATSSPGTLRRFHILIH

901 QEDRSSGSTTELHCVTDERNALRRSS 	1020 LDTPINYGLKYSDEOLI 1020 LDTPINYSLKYSDEOLI	1081 STDDKHLKFOPHFG 1080 STDDKHLKFOPHFG	1141 THYSERYSEEGHEBERRPTHN	1201 SSGQSSKTEHMSSSSENTSTPSSNAKT	TYCVEDTPICFSRCSSISSISSABI	SEVPAVSQHPRTKSSR:	1381 P	1441 PPPOTAGTKREVPKOKAAPTAEKESG 	1501	1561	1621 ONRLOPOKHVSF*PGDDMPRVYCVE	1680 SGEFEKROTIPTEGRSIDEAGGGK 	1741 FRYKKIMOUQQASASSAANKAQL 	1801 AERVFSDNKDSKKON 1800 AERVFSDNKDSKKON	1861	OY 1921 GORVEILGKÖSTPPÖSSKUIPDRCAATDEKL
TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE: ORGANISM: Homo sapiens IMMEDIATE SOURCE: CLONE: APC US-08-289-548A-7	Query Match Best Local Similarity 99.7%; Pred. No. 0; Matches 2835; Conservative 2; Mismatches 5; Indels 1; Gaps 1;	Qy 1 MAAASYDQLLKQVBALKMENSNLRQBLEDNSNHLTKLETEASNMKEVLKQLQGSIEDBAM 60	Qy 61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSRSGECSPVPMGSFPR 120	Qy 121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKOWYYAQLQNLTKRIDSLPLTENFSL 180	Oy 181 QTDLTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240	BARRSSONKHETGSHDAFRQNEGGGVGEINWATSGNGQSSTTRMDHETASVLSSSSTHSA 30	.r.10rr 36 	Qy 361 HGNDKDSVLLGNSRGSKEARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC 420	Qy 421 WEWQEAFEPGMDQDKQIPMPAPVEHQICPAVCVLWKLSFDEEHRHAMNELGGLQAIAELLQ 480	QY 481 VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL 540	QY 541 QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALMNLSAHCT 600 	Qy 601 ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN 660	QY 661 CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQBALWDMGAVSMLKNLIHSKHKMIAM 720	Qy 721 GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS 780	Qy 781 PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNWTVLSPYLATTVLPSSSSRGS 840	QY 841 LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS 900

1020 1019 1080 1079 1140 1139 1440 1740 1199 QLHPSSAQSRSGQPQKAATCKVSSINQETIQ 1260 1320 1319 1380 1379 1439 1500 1499 1560 1559 KGKKPAQTASKLPPPVARKPSQLPVYKLLPS 1620 NFSTATSLSDLIISSPPNBLAAGEGVRGGAQ 1680 1739 1799 1860 SEAKVTSHTELTSNQQSANKTQAIAKQPINR 1920 CLONFAIENTPVCFSHNSSLSSLSDIDQENN 1980 KRHVDQPIDYSLKYATDIPSSQKQSFSFSKS 1200 KKPTSPVKPIPONTEYRTRVRKNADSKNNLN 1800 CQNFAIENTPVCFSHNSSLSSLSDIDQENN 1979 THSNTYNFTKSENSNRTCSMPYAKLEYKRSS DESKFCSYGOYPADLAHKIHSANHMDDNDGE ARPKHIIEDEIKQSEQRAQSRNQSTTYPVYTE KRHVDQPIDYSLKYATDIPSSQKQSFSFSKS NOTTORADSANTLOIAEIKGKIGTRSAEDPV KAVEFSSGAKSPSKSGAQTPKSPEHYVQET SGENVSGIISPSDLPDSPGQTMPPSRSKTPP CSGMVSGIISPSDLPDSPGQTMPPSRSKTPP AAVNAAVQRVQVLPDADTLLHFATESTPDGF SNDNGNETESEQPKESNENQEKEAEKTIDSE KKPTSPVKPIPQNTEYRTRVRKNADSKNNLN THSNTYNFTKSENSNRTCSMPYAKLEYKRSS DESKFCSYGQYPADLAHKIHSANHMDDNDGE SETNRVGSNHGINQNVSQSLCQEDDYEDDKP AAVNAAVQRVQVLPDADTLLHFATESTPDGF IPELDDNKAEEGDILAECINSAMPKGKSHKP NEDRVRGSFAFDSPHHYTPIEGTPYCFSRND SETURVESNHGINQNVSQSLCQEDDYEDDKP KAVEFPSGAKSPSKSGAQTPKSPPEHYVQET

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APPLICANT: MARKHAM, ALEXANDER F.
APPLICANT: NAKAMIRA, YUSUKE
APPLICANT: FILLIVERIS, YUSUKE
APPLICANT: FILLIVERIS, ANDREM
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
TITLE OF INVENTION: GENE IN COLORECTAL CANCER IN HUMANS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, NW
CITY: Washington
STATE: D.C.
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/NS-DOS
SOFTWARE: PATENTIN Release #1.0, Vers
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/452,654
FILING DATE: 25-MAY-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/741,940
FILING DATE: US -MAY-1995
ATTORNEY AGENT INFORMATION:
REJECONFUNICATION NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 32,141
REFERENCE/DOCKET NUMBER: 32,141
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ORIGINAL SOURCE:
ORGANIEM: Homo sapiens
IMMEDIATE SOURCE:
CLONE: APC
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STRANDEDNESS: single
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                                                                                                                                                                                      2040 ECISSAMPKKKRPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2099
                                                                                                                                                                                                                                                                                                                2100 WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT 2159
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2220 MPSISRGRIMIHIPPGVRNSSSSTSPVSKKGPPLKTPASKSPSBGQTATTSPRGAKPSVKS 2279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPN 2339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SFESISPSSRPASPIRSQAQIPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPILEYNDG 2520
              NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ 2040
                                                                                                                                            ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD 2100
                                                                                                                                                                                                                                                                          WKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFT 2160
                                                                                                                                                                                                                                                                                                                                                                                                            SNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKQPLQAN 2220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGISPPN 2340
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US-08-420-654-7
Sequence 7, Application US/08452654
Patent No. 5691454
GENERAL INFORMATION:
APPLICANT: ALBERTSEN, HANS
APPLICANT: ANAND, RAKESH
APPLICANT: CRELSON, MARY
APPLICANT: GRODEN, JOANNA
APPLICANT: HEDGE, PHILIP J.
APPLICANT: USSLYN, GEOFF
APPLICANT: VOSLYN, GEOFF
APPLICANT: KINZLER, KENNETH
              1981
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2641 KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN 2700
2640 KTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDN 2699
                                                                                                                                                                                                                         2701 QAKQNVGNGSVPMRTVGLENRLTSFIQVDAPDQKGTEIKPGQNNPVPVSETNESPIVERT 2760
2520 RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSASSES 2579
                                       2581 SEKAKSEDEKHVNSISGTKOSKENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATNGAES 2640
                                                                                2580 SEKAKKEDDEKHVNSISGTKQSKENQVSAKGTWRKIKENBFSPTNSTSQTVSSGATNGAES 2639
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Search completed: August 25, 2004, 17:25:42 Job time : 53.5 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 25, 2004, 17:06:26; Search time 59 Seconds (without alignments) 4635.127 Million cell updates/sec Run on:

US-09-442-489F-7 14566 1 MAAASYDQLLKQVBALKMEN......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283366 Total number of hits satisfying chosen parameters:

283366 seqs, 96191526 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_78:*
1: Dirl:*
2: Dirl:*
3: Dirl:*
4: Dir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SIIMMARIES

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SUMMARIES		RBHUAP	149505	3025	T13825	1356	9007	3443	2332	2333	4335	451	9520	T02345	3024	2053	8832	4273	3441	3082	4947	2053	3743	C583	1534	1867	8992	T32650	4717	3593
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-4 < LLAM>
A;Cross-references: GB:SS6365; NID:g266243; PIDN:AAD14918.1; PID:g4262770

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ALIGNMENTS

RESULT 1

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	C.batte: 11-Dec-1991 #semisice revision 31-Dec-1991 #text change 21-Jul-2000	
	C. Accession: A37261, B33658; A4928; A49319; I54271	
	R; Kinzler, K.W.; Nilbert, M.C.; Su, L.K.; Vogelstein, B.; Bryan, T.M.; Levy, D.B.; Smith,	ъ,
	chul, S.F.; Horii, A.; Ando, H.; Miyoshi, Y.; Miki, Y.; Nishisho, I.; Nakamura, Y.	
	SCHEMICE 233, 001-003, 1331 Northing 134 (137)	
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	A,Accession: A37261	-
	A; Molecule type: mRNA	
	A)Residues: 1-2843 <kin></kin>	
	Ajtross-references: GB:M/4088; NILDS/glaz.399; FILM:AAAM3380-1; FILM:Jaran B - B - B - B - B - B - B - B - B - B	ž
	Rioskly, G.; Caisou, M.; Millveits, A.; Alleries, F.; Gibert, M.; Goles, M.; Goles, M.; Goles, M.; Caisou, M.; Goles, M.; Le Pastler, D.; Abdersahm, H.; Cohen, D.; Le	i ii
	Cell 66, 601-613, 1991	4
	A,Title: Identification of deletion mutations and three new genes at the familial polypos	š
	A;Reference number: A39658; MUID:91330307; PMID:1678319	
	A;Accession: B39658	
	A; Molecule type: DNA	,
	A)Residues: 1-183,'L',185-969,'N',971-1308,'G',1310-1324,'SS',1326,'HSTLE',1332-1354,'F',	
	A;Cross-references: GB:M73548; NID:14460195; PIDN:14460196:1; PID:19190106 N. W. V. V. V. V. V. V. V. V. V. V. V. V. V.	÷.
	rya, U., Minister,	í
-	Cancer Res. 52, 043-043, 1992. Annuel Res. 12, 043-043, 1992. Annuel Res. 12, 043-043, 1992.	ŭ
	A/Accession: A44928	
	A; Molecule type: DNA	
	A; Residues: 1506-1525 < MIK>	
	*)Cross-references: GB:S78214; NID: 254.3541; PIDN:AA521145:1; PID:243.542	
	A)Note: Sequence extracted those backbone (Note:) activity of the Collection of the	ţ
	Kisbillo, Li, Olschwang, S.; Groden, U.; Robertson, M.; Samowitz, M.; Ocelyn, G.; Gerbon	,
	A: Title: Alleles of the APC gene: an attenuated form of familial polyposis.	
	A; Reference number: A49319; MUID:94073973; PMID:8252630	
	A;Accession: A49319	
	A;Status: preliminary; translated from GB/EMBL/DDBJ	
	A; Molecule type: mRNA	
	A;Residues: 'G',143-171,'P',173-179 <spi></spi>	
_	A;Cross-references: GB:S67787; NID:g461061; PIDN:AAD13997.1; PID:g4261697	
-	R;Lambertz, S.; Ballhausen, W.G.	
	Hum. Genet. 90, 650-652, 1993	5
	A)TITIE: IQENTILIZATION OF AN AITEMBALIVE S. UNITARISATEM LEGION OF THE AUGMANDES PORT	4
	Affeterementer indumer: 1542/1; NOID:9510019/; FRID:0505074	
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C;Genetics: A;Gene: GDB:APC A;Cross-references: GDB:119682; OWIM:175100 A;Map position: 5q21-5q22 A;Map position: 5q21-5q22 A;Map position: 5q21-5q22 A;Map position: 5q21-5q22 A;Map position: 6q21-5q22 A;Map position: 6q21-5q22 A;Map position: 6q21-5q22 A;Map position: 6q21-5q22 C;Reywords: cancer; familial adenomatous polyposis; tumor suppressor C;Reywords: cancer; familial adenomatous polyposis; tumor suppressor F;7-72/Region: coil #status predicted F;135-227/Region: coil #status predicted F;131-1156/Region: acidic F;131-1156/Region: acidic F;1866-1893/Region: highly charged	Query Match 100.0%; Score 14566; DB 1; Length 2843; Best Local Similarity 100.0%; Pred. No. 0; Matches 2843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	QY 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 60 	QY 61 ASSGQIDLLERLKELNILDSSNPPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 120	7	OTDMTRROLEYBARQIRVAMBEQLGTCQDMBKRAQRRIARIQDIBKDILRIRQLLGSQAT 2	241 BAERSSONKHETGSHDAERQNBGQGVGBINMATSGNGQGSTTRMDHETASVLSSSSTHSA	301 PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLFLLIQLL 3 301 PRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLFLLIQLL 3 301 PPRLTSHLGTKVEMVYSLLSMLGTHDKDMSDF113MCSGCLSMGSGCC1.	361 HGNDKDSVLLGNSRGSKEARARASAALHNIHSQPDDKRGRREIRVLHLLEQIRAYCETC 4	421 WEWOEAHEPGYDOKKYPMPAPVEHOICPAVCYLMKI.SPDEHRHAMYELGGIOAIAELLO 48 421 WEWOEAHEPGYDODKYPMPAPVEHOICPAVCYLMKI.SPDEHRHAMYELGGIOAIAELLO 48 421 WEWOEAHEPGYDODKYPMPAPVEHOICPAVCYLMKI.SPDEHRHAMYELGGIOAIAELLO 48	481 VDCENYGLTNDHYSTTLRRYAGMALTNLTFGDVANKATLCSMKGCNRALVAGLKSESEDL	541 OOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALMNLSAHCT	601 ENKADICAVDGALAFLYGTITYRSOTNTLAIIESGGGILRNVSSLIATNEDHROILRENN 601 ENKADICAVDGALAFLYGTITYRSOTNTTAIIESGGGTIRNVSSTIATNEDHROILRENN 601 ENKADICAVDGALAFLYGTITYRSOTNTTAIIESGGGTIRNVSSTIATNEDHROILRENN	661 CLOTLLOHLKSHSLTIVSNACGTLWNLSARNPKODEALWDMGAVSMLKNLIHSKHKMIAM [NIDNES 78	781 PKASHRSKQRHXQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLMTTVLPSSSSSRGS 84

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RESULT 2
149505
adenomatous polyposis coli protein - mouse
N;Alternate names: APC
C;Species: Mus musculus (house mouse)
C;Date: 02-7ul-1996 #sequence_revision 02-7ul-1996 #text_change 13-Aug-1999
C;Accession: 149505
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of the R;Su, L.
Science 256, 668-670, 1992
A;Title: Multiple intestinal neoplasia caused by a mutation in the murine homolog of A;Title: Multiple intestinal neoplasia caused by a mutation in the murine homolog of A;Reference number: 149505; MUID:92263101; PMID:1350108
A;Recession: 149505
A;Mulecule type: mRNA
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-2845 cRES
A;Cross-references: GB:MS8127; NID:91991; PIDN:AMB59632.1; PID:91992.
C;Superfamily: adenomatous polyposis coli protein 780 900 10 420 418 480 478 540 538 600 598 660 658 720 718 778 840 120 118 180 178 240 238 300 298 360 358 9 9 GSAAALRNIMANRPAKYKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS PKASHRSKQRHKQNLYGDYAFDANRHDDSRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGS LDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEEVSAIHTS 61 -TSGQIDILERIKEFNLD-SNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT QTDMTRRQLEYEARQIRAAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRVRQLLQSQAA PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSGCLPLLIQLL 359 HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIABLLQ VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM GSAAALRNIMANRPAKYKDANIMSPGSSLPSIHVRKQKALEAELDAQHISETFDNIDNIS PKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNNTVLSPYLNTTVLPSSSSSRGS 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM 1 MAAASYDQLLKQVEALKGVENSNLRQELEDNSNHLTKLETEASNMKEVLKQLCGSIEDETM EAERSSONKHETGSHDAERONEGOGVGEINMATSGNGOGSTTRMDHETASVLSSSSTHSA PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC VDCEMYGLTNDHYSVTLRRYAGMALTNLTFGDVANKATLCSMKGCMRALVAQLKSESEDL QQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAHCT 61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR Gaps 12; 2845; Length Indels DB 2; 155; Query Match 90.5%; Score 13178; I Best Local Similarity 90.2%; Pred. No. 0; Matches 2572; Conservative 111; Mismatches 779 419 479 539 599 629 721 719 781 121 119 179 241 239 301 299 361 421 481 541 601 199 841 181 D CY $\dot{\delta}$ 8 % 8 දු පු ò g à 8 B 8 셤 8 8 $\dot{\delta}$ 엄 g ò 셤 à В 임 à જે

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LDSSRSEKDRSLE	901 QEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLEYKRSS 960 	961 NDSLNSVSSSDGYGKRGQMKPSIESYSEDDESKRCSYGQYPADLAHKIHSANHMDDNDGE 1020	1021 LDTPINYSLKYSDEQLNSGRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTYPVYTE 1080 	1081 STDDKHLKFQPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKP 1140 	1141 TNYSERYSEEDH-EEEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSK 1199 	SSGQSSKTEHMSSSSENTSTPSSNAKRONOLHPSSAOSRSGOPOKAATCKVSSINOETI 125	1260 QTYCVEDTPICFSRCSSLSSAEDBIGCNQTTQEADSANTLQIABIKEKIGTRSAEDP 1319 	1320 VSEVPAVSQHPRTKSSRLQGSSLSSESARH-KAVEFSSGAKSPSKSGAQTPKSPFEHYVQ 1378 	1379 ETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRKT 1438 :	PPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPD 14	1499 GFSCSSSLSALSLDEPPIQKDVELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTID 1558 	SEKOLLDDSDDDIEILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLL 161 	PSQNRLQPQKHVSFTPGDDMPRVYCVBGTPINFSTATSLSDLTIESPPNBLAAGBGVRGG 167 :	1679 AQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSH 1738 	1739 KPFRVKKIMDQVQQASASSSAPNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNN 1798 	1799 LNAERVFSDKKONKKONLKONSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSR 1858 	1859 NDSLSSLDFDDDDVDLSREKAEIRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPI 1918 	1919 NRGQPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQE 1978 : :
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oque of the adenomatous polyposis coli tumour sur 6; PMID:10021369, Wetering, M.; Molenaar, M.; Miles, A.; Kuipers, SSESKGIKGGKKVYKSLITCKVRSNSEISGQMKQP 2216 ISPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSE 2097 2276 2336 NRLNSFIQVDAPDQKGTEIKPGQNNPVPVSETNE 2753 ||||||:||||||||||||||||| TRLNSFVQVEAPEQKGTEAKPGQSNPVSIAETAE 2755 ASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD 2036 CLSRQASSDSDILSLKSGISLGSPFHLTFDQEE 2156 TSPVSKKGPPLKTPASKSPSEGOTATTSPRGAKP 2276 2336 2396 2456 RRGTWKREHSKHSSSLPRVSTWRRTGSSSILSA 2576 ENQVSAKGTWRKIKENEFSPTNSTSQTVSSGATN 2636 2696 RVTPPNYNPSPRKSSADSTSARPSQIPTPVNNNT 2813 ASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD 2037 CLSROASSDSDSILSLKSGISLGSPFHLTPDQEE 2156 KMSYTSPGRQLSQQNLTKQASLSKNASSIPRSES 2396 KSSGSESDRSERPVLVROSTFIKEAPSPTLRRKL 2456 VLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIE 2516 VLSPSLPDMSLSTHPSVQAGGWRKLPPNLSPTIE 2516 DCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKD 2696 2-Oct-1999 #text_change 21-Jul-2000 SSRDSTPSRPAQOPLSRPIQSPGRNSISPGRNGI KMSYTSPGROMSQQNLTKQTGLSKNASSIPRSES KSSGSESDSSERPALVRQSTFIKEAPSPTLRRKL DCPINNPRSGRSPTGNTPPVIDSVSEKGSSSIKD GSRDSTPSRPTQQPLSRPMQSPGRNSISPGRNGI ||||| VTSV 2845 VTSV 2843 onse

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                                                                                                            KFCSYGQYPADLAHKIHSANHMDDNDGELDTPINYSLKYSDEQLNSGRQSPSQNERWARP 1052
                               887
    KRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNT
                     PSSAQSRSGQPQKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQT
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                                                          YNFT - - KSENSNRTCSMPYAKLEYKRSSNDSLNSVSSSDGYGKRGQMKPSIESYSEDDES
                                                                                                                                                                KHI I EDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSPYRSRGANGSET
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A;Gene: APC2
A;Introns: 47/3; 78/1; 138/2; 174/3; 212/3; 238/3; 271/3; 396/1; 428/1; 474/3; 500/3;
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                                             A;Residues: 1-2274 <VAN>
A;Cross-references: EMBL:AJ130783; NID:g4210431; PIDN:CAA10207.1; PID:g4210432
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                                                                                                                                                                                              QTDWTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDIL----RIRQ---
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                                                                                                                                                     Indels 779; Gaps
                                                                                                                           DB 2; Length 2274;
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ilarity 34.3%; Pred. No. 6.3e-136;
Conservative 354; Mismatches 788;
Accession: T30258; status: preliminary; translated from GB/EMBL/DDBJ: Molecule type: DNA
                                                                                                                          Query Match
Best Local Similarity
Matches 1005; Conserv
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D:97144426; PMID:8990193

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A; Reference number: 217782; MUID A; Accession: T13825 A; Status: preliminary; translate A; Molecule type: mRNA, A; Residues: 1-2416 (HAY) A; Cross-references: EMBL:U77947; C; Genetics: A; Genetics: A; Gross-references: FlyBase:FBgn A; Map position: 3R	Query Match Best Local Similarity 25.4%; Matches 720; Conservative 3	Qy 243 ERSSQNKHETGSHDAERQ : : Db 129 ELREMREHRSLDRNFERQ	Qy 296 STHSAPR	Qy 338 SSSQDSCISMRQSGCLPL : : : Db 249 SGNAQSCATLRRSGGMPL	Qy 398 KRGRREIRVLHLEGIRA 	OY 456 LSFDEEHRHANNELGGLO. 	Qy 515 NKATLCSMKGCMRALVAQ 	Qy 575 CALEVKKESTLKSVLSAL) :	Qy 635 GGGILRNVSSLIATNEDHI	Qy 695 QEALWDWGAVSMLKNLIH 	Qy 750 PSLHVRKQKALEAELDAQ)	QY 810 RSDNFNTGNMTVLSPYLAY Db 678TGG	QY 870 PGTSSKRGLQISTTAAQI) :	QY 930 THSNTYNFTKSENSNRTC	Db 726	Qy 990 DESKFCSYGQYPADLAHK:	1050
	Qy 2091 GLSPDSENFDWKAIQEGANSIVSSLAQAAAACLSRQASSDSDILSLKKGISLGSPF 2148	QY 2149 HLTPDQEEKPFTSNKGPRILKPGEKSTLETKKI-BSESKGIKGGKKVYKSLITGKVR-SN 2206 DD 1702 QPSKLRKGRKPAABAGGAMRPEKRGTTSTKINGSPRLPN 1740	OY 2207 SEISGOMKOPLOANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGOT 2266 DD 1741 GPEKAKGTOKMAGESTWLRGRIVIXSAGPASRTOSKGISGPCTTPKKTGTS 1792	QY 2267 ATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGRDSTPSRPAQQPLSRPIQSPGR 2326	OY 2327 NSISPGRNGISPPNKLSQLPRISSPSTASTKSSGSGKMSYTSPGRQMSQON 2377 1832 SATPPARLAKTPSSSSSQISPASQPLPRRSPLATPTGGPLPGPGGSLVPKSPRARL 1887	QY 2378 LIKQTGLSKNASSIPRSESASKGLNQMNNGNGA-NKKVELSBMS 2420	OY 2421 STKSSGSSEDRSERPVLVRQSTFIKEAPSPTLRRKLEBSASFBSLSPSSRPASPTRSGAQ 2480 	QY 2481 TPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKHDIARSHSESPS 2537 DD 2005 LPAVFLCSSRCDELRVSPRQPLAAQRSPQAKPGLAPLAPRRTSSESPS 2052	QY 2538 RLPINRSGTWKREHSKHSSLPRVSTWRRTGSSSSILGASSESSEKAKSEDEKHVNSIS-2596 DD 2053 RLPV-RASPGRPETVKRYASLPHISVSRRSDSAVSVPTTQANATRRGSDGEARPLPRVAP 2111	Qy 2597 -GTKQSKENQVSAKGTWRKIKENBFSPINSTSQTVSSGAINGAESKTLIYQMA 2648	OY 2649 PAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNV 2706	Qy 2707 GNGSVPMRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPFSSSS 2766 Db 2189ASGPVAPQGSDVDGPVLTKPPASAPFPHEGLSAVIAGFP 2227	QY 2767 SSKHSSPSGTVAARVTPPNYNPSPRKSSADSTSARPSQIPTPVN 2810			a melanogaster fig. (1999 #text_c)	R'Hayashi, S.; Rubinfeld, B.; Souza, B.; Polakis, P.; Wieschaus, E.; Levine, A.J. Proc. Natl. Acad. Sci. U.S.A. 94, 242-247, 1997 A;Title: A Drosophila homolog of the tumor suppressor gene adenomatous polyposis coli dd

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                                            ; NID:g1800228; PID:g1800229; PIDN:AAB41404.1
                                                                                                                                                                                                                                                                                                                     ---RLTSH-----LGTKVEMVYSLLSMLGTHDKDDMSRTLLAM
                                                                                                                                                                                                                                                                              OAIAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA
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|-----QDTEATEEQPIDYSVKYS-------
                                                                                                                                                                                                QN-EGQGVGEINMATSGNGQGSTTR-----MDHETASVLSSS
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                                                                                                                                     ; Score 1780.5; DB 2; Length 2416;
; Pred. No. 5.3e-65;
329; Mismatches 847; Indels 935; Gaps
                                                                                                                                                                                                                                                                                                                                                                                   AYCETCWEWQEAHEPGM--DQDKNPMPAPVEHQICPAVCVLMK
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ed from GB/EMBL/DDBJ
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RHTAETCDNLD-----
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Ω	1509	KSKEPSRRESIAESLKAESTKDEKSAPPSKEASRPGSVVESVKDETEKS	1557
>-	760 LEAEL	DAQHLSETFDNIDNLSPKASHRSKQRHKQSLY	819
Ω	1558 KEP	SRRESIAESAKPPIEFREVSRPESVIDGIKDESAKPESRRD	1601
>-	820 TVL	SPYINTTUDESSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGT	872
Ω	1602	PES	1652
>-	873 SSK	H	932
Д	1653 SK-	SMSKEPS	1694
>-	933 NTYN	FIKSENSNRICSMPYAKLEYKRSSNDSLNSVSSSDGYGKRGQMKPSIESYSED	686
Q	1695 RRE	SVKDGAAQSKETSRPASVAĖSAKDGADDLKELSRPEŠTTQSKEAGSIKDEKSPLASE	1754
>-	990 DESI		1038
۵	1755 EAS	EASRPASVAESVKDEAEKSKEESRRESVAEKSPLPSKEASRPASVAESIKDEAEKŠKEES	1814
>-	1039	GRQSPSQNERWARPKHIIEDBIKQSEQRQSRNQSTTYPVYT	1079
Ω	1815 RRE		1874
>-	1080 EST		1132
۵	1875 ESI	AEKSPLPSKEASRPASVAESIKDEAEKSKEESRRESVAEK	1933
خ ر	1133 D	IDYSLKYATDIP	1188
۵	1934 SPL	PLPSKEASRPASVAESIKDEAEKSREESRRESVAEKSPLPSKEASRPASVA	1985
>-	1189 SSQ1		1240
Ω	1986 ESII	I IKDBABKŠKEEŠRREŠVAĒKSPLPŠKEAŠRPAŠVĀESIKDBABKSKEEŠRREŠVAĒKS	2045
> -	1241 GQP(29
۵	2046 PLP	4	2103
>-	1290 NQTTQE	ADSANTLQIABIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQG	1339
۵	2104 DKS	DKSKBESRRESMAESGKAQSIKGDQSPLKEVSRPESVAESVKODPVKSKEPSRRESVA	2161
>-	1340 SSLS:	SESARHKAVEFSSGAKSPSKS-GAQTPKSPPEHYVQETPLMPSRCTSVSSLDSFES	1398
۵	2162 GSV	ADSARDDOSPLESKGASRPESVVDSVKDEABKQESRRES	2204
>-	1399 RSI	ASSVQSEPCSGMVSGIISPSDLPD-SPGQTMPP-SRSKTPPPPPQTAQTKR	1450
۵	2205	IREDADOPMKPSQAESRR	2250
>-	1451 E	TAEKRESGPKQAA VNAAVQRVQVLPDADTLLHFATESTPD	1498
۵	2251 ESIAE	SIKASSPRDEKSPLASKEASRPGSVAESIKYDLDKPQIIKDDKSTEHSRRESLED	2310
>-	1499 GFS(SISSIS	1507
۵	: : 2311 KSAVT	 SEKSVSRPLSVASDHEAAVAIEDDAKSSISPKDKSRPGFVAETVSSPIEEATMEF	2370
>-	1508	Σ.	1525
۵	2371 SKII	EVVEKSSLALŠLOGGSGGKLQTDSSPVDVAEGDFSHAVASVSTVTPTLTKPAELAQI	2430
>-	1526	۵	1569
۵	2431 GAA		2490
_	1570 DDII		1617
0	2491 DDA	DDAAQLKSSVEDLRSPVASTEISRPASAGETASSPIEEAPKDFAEFEQAEKAVLPLTIEL	2550

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1618LBSQNRLQPQKHVSFTFGDDMPRVYCVEGTPINFSTATSLSDLFIESPPNELA 1670	1671 AGEGVRGGAGSGEPEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEE 1720 	PPS	PNKNQLDGKKKKPTSPVKDIPQNTEYRTRVRKNA 	1794 DSKNNLNAERVFSDNKDSKKQNLKNNSKDFNDKLPNNEDRVRGSFAFDSPHYTPIEGTP 1853 	1854 YCFSRNDSLSSLDFDDDDVDLSR	1894 VTSHTELTSNQQSANKTQALAKQPINRGQPKPILGKQSTFPQSSKDIPDRGAATD 1948	1949 EKLONFA 1974 :	1975IDQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPV 2019 2998 DEKSLLVSQEASRPESEAESLKDAAAPSQETSRPESVTESVTGSVKDGKSPVASKE 3049	2020 CFSRNSSLSSLSIDSEDDLLQECISSAMPKKKRPSRLKGDNEKHSPRNMGGIL 2072	2073 GEDLTLDLKDIQRPDS-EHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSD 2131 	2132 SDSILSLKSGISLGSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGG 2191 	2192 KKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSSSTSPVSK 2248 :	2249 KGPPLKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRD 2306 :	2307 STPSRPAQQPLSRPIQSPGRNGISPGRNGISPDNKLSQLPRTSSPSTASTKSSGSGKMSY 2366 1:	2367 ISPGROMSQONLTKQTGLSKNASSIPRSESASKGLNOMNGNGANKKVELSRMSSTKSSG 2426 3351EBSRRESVAEKSPLASKEASRPTSVAESVKDEAEKSKEESSRDSVAEKSP 3400	2427 SESDRSERPVLVRQSTFIKEAPSPTLRRKLEESASFESLSPSSRPASPTRSQAQTPV 2483 1401 LASKEASRPASVAESVQDEAEKSKEESRRESVAEKSPLASKEASRPASVAESVKD 3455	2484 LSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSBSPSR 2538 3456DAEKSKEESRRESVAEKSPLASKEASRPASVAESVKDEAEKSKEES 3501	
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tical protein SA2447 [imported] - Staphylococcus aureus (strain N315)
10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
sion: F90073
1a, Mr. Ohtan, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguch
inba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
357, 1225-1240, 2001
1: Whole genome sequencing of meticillin-resistant Stapylococcus aureus.
inche number: A88758; MuID:21311952; PMID:1141846 2710 SVPMRTVGLENKLNSFIQVDAPDQKGTEIKPGQNNPVPVSFINESSIVERTPFSSSSSSK 2769 3651 ----RESGAEKSPLASMEASRPTSVAESVK--DETEKSKEESRRESVTEKSPLPGKEASR 3704 2770 HSSPSGTVAARVTPFNYNPSPRXSSADST----SARPSQIPTPVNNNTK--KRDSKTD 2821 75; KOSKENOV--SAKGTWRKIKEN-----EFSPTNSTSQTVSSGATNGAESKTLIYQMAP 2649 s: preliminary ule type: DNA ues: 1-221 «KUR» -references: GB:BA000018; PID:g13702612; PIDN:BAB43752.1; GSPDB:GN00149 imental source: strain N315 2539 LPINRSGTWIREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGT 2598 706 461 753 808 923 624 TNSIIGTPTKIG------QSTVTVVSTDQANNKSTTTFTINVVDTTAPTVTPI 670 606 ICAVDGALAFLVGTLIYRSQTWTLAIIE-----SGGGIL------RNVSSLI 646 462 SGTTNFSLSMTASTGGATNLQQVQFGTFEXTESAVIQVRYVDVTTGKDIIPPKTYSGNVD 521 647 ATNEDHROILRENNCLOTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSM 754 V-----RKOKALEAELDAQHLSETFDNIDNLSPKASHRSKORHKOSLYGDYVFDTNRHDD 809 NRSDNFNTGNMTV-LSPYLNTTVLPSSSSSRGSLDSSRSEKDRSLERERGIGLG-NYHPA 353 İGGLSNAFGFKLDİYHNTSKPNSAAKANADPSNVAĞĞARĞAFGAFVTTDSYGVATTYTSST 707 LKNLIHSKHKMIAMGSAAALRNLM-----ANRPAKYKDA----NIMSPGSSLPSLH 867 TEN-PGISSKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALR--3.5%; Score 517; DB 2; Length 2271; Local Similarity 19.5%; Pred. No. 2.5e-13; es 450; Conservative 332; Mismatches 1013; Indels 514; Gaps Length 2271; 3764 SMPESG 3769 2822 STESSG 2827 SA2447 3502 2599

924RSSAAHTHSNITYNFTKSENSNRICSMPYAKLEYKRSSNDSLNSVSSSDGYGKRGQMKP 981 : : : : : : : : : :	λό g	1976 DQENNNKENEPIKETEPPDSQGEPSKPQASGYAPKSFH
SIESYSEDDESKFCSYGQYPADLAHKTHSANHMDNDGELDTPINYSLKYSBEQLNS 10	8	
	g &	1639 QSMSL8TSTSTSMSDSTSLS
1039 GRQSPSQNERWARPKHIIEDEIKQSEQRQSRNQSTTXPVYTESTDDKHLKFQPHFGQGEC 1098 761 GSTQQSQSV9TSKADSQSATSTSGSITVSTSAGTSKSTSVSLSDS 806	ga qa	
VSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEEGHEEEER	ò 8	2155 BEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGCK
PINYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSSGQSSKTEHMSSSSENT 1	\$ B	2212 QWKQPLQANMPSISRGRIMIHIPGVRNSSSSTSPVSKK
SLSTSTSDSLRTSTSDSLSMSTSGSLSKSQSLSTSISGS	8	RGAKPSV
 1219 SIPSENAKKONULAPSEKAKSKOQPOKAAICKVSSINQETIOTYCVBDTPICFSKOSS 1276	qq	1802 SGSTSTSTSGSLSTSTSLSGSESVS
1277 LSSLSSAEDEIGCNOTTQEADSANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSBR 1336	à a	2331 PGRNGISPPNYLSQLPRISSPSTASTKSSGGKMSYIS
LQGSSLSSESARHKAVEFSSGAKSPSKSGAQ-TPKSPPEHYVQETPLMFSRCTSVSS 139	<u>ک</u> و	2391 IPRSESASKGLNOMNNGNCANKKVELSRMSSTKSSGSE
LEASUSKSMSVSSSMSTEGSGSTSESLEDSGSTSDSDSKELSLSTGGSGS LDSFESRSIASSVQSEPCSGMVSGIISPSDLPDSPCGTMPPSRSKTPPPP : :	දි සි	2451 TLRRKLEBSASFESLSPSSRPASPTRSQAQTPVLSPS- :
VRISESQSTSGSMSASQSDSWSISTSFSDSTSDSKSASTASSESISQSASTSTSG 113 PKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLS 150	\$ B	2510 NLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTW 1:
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123	\$ A	2630 VSSGATNGABSKTLIYQMAPAVSKTEDVWVRIEDC 1
RIQPOKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSG 16	ك	2687 SEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLNS
1290 SISANISLELSINGEDSISDENGEDSISHSISDELSISKEDSISISISSES 1344 1683 EFERRDIIPTEGRSTDEAQGRKISSVIIPELDDNKAEEGDILAECINSAMPKGK 1736 1345 ESDSTSSESKESKEDTSMSISMSQSTSGSTSISTSTSELSISASMNQSG 1399	QY	2747 PVSETNESSIVERTPFSSSSSKHISSPSGTVAARVTPF:
SHKPFRVKKIMDQVQQASASSAPNRNQLDGKKKKRPTSPVKPIPQNTEYRTRVRNADSK 179	ò q	2807 IPVNNNTKKRDSKIDSTESSGTQSPKR 2833 : : : : 2200 ISTSESQSTLSATSEVIKHNGTPAQSEKR 2228
1797 NNLNAERVESDNKDSKKONLKNNSKDFNDKLPNNEDRVRGSFAPDSPHHYTPIEGTPYCF 1856 : : : : 137 1437 ESTSTSTSISDSTSTSKSSOSGSTSTSTSSSSSSSSSSSSSSSSSSSSSSS	RESULT T34434	ı- †
SRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQ	C;Spec C;Date C;Acce	n 29-0ct-199
SLSDSTSTSNGGSASTGTSLSNSASASESDSSGTSLSDSTSASMQSSESDS PINRGQPKPILQKQSTFPQSSKDIPDRGAATDEXLQNFAIENTPVCFSHNSSLS-SLSDI	R, Geiss submit A; Desc A; Refe	RiGeisel, C.; Gattung, S. submitted to the EmBL Data Library, December 1996 A; Description: The sequence of C. elegans cosmid KO6/A; Reference number: Z21525
1545QSTSASLSDSLSTSTSNRMSTIASLSTSESGSTSESTSES 1588	A, Acce. A, Stati	ssion: T34434 us: preliminary, translated from GB/EMBL/DDBJ

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2034
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STSTSGSLSTSTSLSGSESVSESTSLSDSISMSDSTSTSDSDSL 1849
                                                                                           KKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSP 2094
                                                                                                                                         ----- DSVSDSTS 1666
                                                                                                                                                                                                                     KPGEKSTLETKKIESESKGIKGGKKYYKS---LITGKVRSNSEISG 2211
                                                                                                                                                                                                                                                                                                                               -----ESDSKSMSGSTSVSDSGSLSVSTSLRKSESVS- 1754
                                                                                                                                                                                                                                                                                                                                                                                RGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSEGQIATISP 2271
                                                                                                                                                                                                                                                                                                                                                                                                              GSQSM--SDSVSTSDSSSLSVSTS---LRSSESVSESDSLSDSKST 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSIS- 2330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LPRISSPSTASTKSSGSGKMSYTSPCROMSQONLTKQTGLSKNASS 2390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SDSLSDSKSLSSSQSMSGSES-TSTSVSDSQSSSTSNSQF--DSMS 1906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSP 2450
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGS 2569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPTNSTSQT 2629
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ò	1838 FAFDSP	AFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELTKAKENKESEAKV 1894
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Š	2001 KPQASGYAPKS	FHVEDTPVCFSRNSSLSSLSIDS
Dþ	1636 VPAWEGE	VPAWEGKSPEGEVRYWRDRDITLQQDAYWRELSCDRKVWFPHELDGQGARPRYCEEREST 1695
ò	2056 LKGDNE	KHSPRNMGGILGEDLTLDLKDIQRPDS
QQ	1696 FLDEGF	GPDEQEITPLQHTPRSPWTSDFKDFQEPLPQKGLEVERWLA 1740
ò	2108 ANSIVS	IVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPF 2159
QQ	1741	
ò	2160	-TSNKGPRILKPGEKSTLETKKIESESK
Db	1764 PPASPPE	:
λŏ	2187	GIKGGKKVYKSLITGKVRSNSFISGOMKOPLQANMPSISRG 2227
qq	1822 PLSPAP	PLSPAPAPPTPAPEPHTPVPFSWGLAEYDSVVAAVQEGAAELEGGPYSPLGKDYRKAEGE 1881
ò	2228 RTMIHIE	TIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSE 2263
QU	1882 REGEGG	
oy.	2264GQT	GQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTP 2309
q	1942 LTGLGPA	LTGLGPACPTREPPLGASGDWPPHLSTKEEAAGCNTSAEKETSSPASPQNLGSDTPAFSY 2001
ģ	2310SRP#	SRPAQOPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRISSPST 2353
qq	2002 ASLAGPA	ASLAGPAVPRQEPDPGPNVEPSITPPAVPPRAPISLSKDLSPPLNGSTVSCSPDRRT 2059
δγ	2354 ASTKSSG	ASTKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRSESASKGLNQMNNGNGA 2410
qq	2060 PSPKETGRGHW-	SEGHWDDGTNDSDLEXGAREQPEKETRSPSPHHPMPMGHSSLW 2108

677GLEISAADLAGSGSGITLPTTLEPKIEGSGKKASGGVWTEEDEGEDEDLM 726	1156 RERPTINYSIKYN 1176			787 SDGEEKLTVEKDGKEAQSSGSSATSSGKKSEATSGSSSSSAKSGTGSEASGSSGASSSG 846	1237 OSRSGOPOKAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSAEDEIG 1288	847 SGVSGESGSSVSTESGSFGTSSSGSVGSEATGSTGVDGSESGKPSKSSTEEKLP 900	Š			953 HPESGSKVSVTSGKGPTQSGAEGSGSGPKVPKGPGAPEITTDGEESSSTSTGD 1005		106	SR 143		aavnaav	1124 - KTEDKSSETPOLGLEISAGKKPEPEDGTSKEVGLEILWESTTPGSTT 1170		1171 LDSDSVGLEISGSDLTKATKKPHVEIEGSGTGDEEITATTRÖVSKSTKKPRVEVDGGDNG 1230		1231 BTSGVDGKPTTPAPTPSSSAESSTSRIPTTSEASPEGGSGEAGVPESPDGSGESSTSAPD 1290		PSTEVTSPEGSGT		1349 EESTLPPTEGSGESTTSSAPTVEPATVLPPQNRNEKPEPTKDTFALPTTTTGAPQAN 1405		DSSVENTKCTSSDECGLDALCERTGVCRCEPGFEGAPPKKSCVDVDECATGDHNCH		ICCGANAKCVNKPGTYSCECE		CKECMĠĠŸKKSĠKV	VKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDSKKQNLKNNSK	CEDINECVAEKAPCSINANCV	CEDVEKFCGRVDHVSCLSVRIYNG	1861 SLSSLKENKESEA 1892	: : :
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OV 2411 NKKVELSRMSSTKSSGSESD 2430		T	2169 FALALVPGTPTRTRHDEYLEVTKAPSLDSSLPQLP8PSSPGGPLLSNLPRPASPALSEGS	Qy 2476 RSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRP 2522	Db 2229 SSEATTFVISSVAERFFPGLEAAEQSAEGLGSGKESAAHSLWDLTPLSPAP 2279	Qy 2523 AKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSS 2571	Db 2280 SASLDLAPAPAPAPAPAPAPAGLPGDLGDGTLPCRPECTGELTKKPS 2323	ENQVSAKG	Db 2324 PFLSPSGDHEANGPGETSLNPPGFVTATAEKEEAEAPHAWERGSWPEGAERSSRPDTL 2381	QY 2625 -STSQTVSSGAINGAESKTLIYQMAPAVSKTEDVWV 2659	Db 2382 LSSEQPLRPGKSSGGPPCSLSSEVEAGPQGCATDPRPHCGELSPSFLNPPLPPSTDDSDL 2441	QY 2660 RIEDCPINNPRSGR-SPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMR 2714	DD 2442 STEEARLAGKGGRRRVGRPGATGGPCPMADETPPTSASDSGSSQSDSDVPPETEECP 2498	OY 2715 TVGLENRLNSFIQVD-APDQKGT-EIKPGQNNPV	Db 2499 SITAEAALDSDEDGDFLPVDKAGGVSGTHHPRPGHDPPPTPLPDFRPSPPRPDVCWADPE 2558	OY 2749 SETNESSIVERTPFSSSSSSKHSSPSGTVARRVIPFNYNPSPRKSSADSTS 2799	DD 2559 GLSSESGRVERLREKGRPGRRAFGRAKPASPARRLDIRGKRSPIPGKGPVDRISRIV 2615	QY 2800 ARPSQIPTPVNNNTKK 2815	Db 2616 PRPRSTPSQVTSAEEK 2631			Aypothetical protein 28.83.1 - Lagundinabultis elegans C;Species: Caenothabditis elegans elegans C;Species: 0.001 1000 morning 20.001-1000 #text chance 20.001-1000	00 17 36mm 200 1 1000	1994	A; Description: Ine sequence of C. elegans cosmin antos. A; Reference number: 221536 a. Accession: T34513	A.Status: preliminary; translated from GB/EMBL/DDBJ	4418.1.	clone ZK783	Cydenectos: A)Gene: CSSP: ZK783.1	A; Map position: 3 A; Introns: 14/1, 48/2, 84/1, 196/3, 303/1, 381/1, 586/1, 605/1, 1175/3, 1207/1, 1409/2;	Match 3.1%; Score 454;	Similarity 19.9%; Pred. No. 1.7e-10; 5; Conservative 277; Mismatches 849; Indels 7.	IKQSEQRC		Qy 1100 SPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKFTNYSERYSEEEQHEB 1155

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KVTSHTELTSNQQSANKTQALAKQPINKGQPKPILQKQSTFPQSSKD 1939	QECISS	PASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQIGGSSKAPS 230 :: : : :	FIKEAPSPTLRRKLEBSASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSL 2493 LINSBEPSTTEAPTTLSPDILSTTTNNLSQSSTVSTEDRSEISSENSEKPTSAPELVTSSV 2384 STHSSVQAGGWRKLPPNLSPTIEYNDGRPAKHDIARSHSESPSRLPINKS 2544 -	TNSTSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNP-RSGRSPTGN 2678 KESESTTTSSESSKPSQEPAGLITSTVVVPTSSLITASIEAHTSNTPFKQGRTPITT 2603 TPFVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMRTVGLENRLNSFIQVDAPD 2732
1893 KVTSHTELTSNQQSANKTQZ : : : : : : : : : : : : : : : : : : :	2040 QECISS	2248 KKGPPLKTPASKSPSEGGTP 2100STPSTTSGSVT 2301 RSGSRDSTPSRPAQQPLSRE 2151 TTGDTNSTTPSTSS 2354ASTKSSGSGKMSYT 2205 ESSTVQASETSGTSSGTSSTSSTS 2397ASKGTMQMINGN 2397ASKGTMQMINGN	2443 FIKEABGPTLRRKLEE 2325 INSERPSTTEAPTTLSPDIL 2494 STHSSVQAGGRRKLPPNLSP 2385 -THVASSSP 2545 GTWKREHSKHSSSLPRVSTW 2545 GTWKREHSKHSSSLPRVSTW 2540 TTASEEPTKSTSMSPDLST	2623 TNSTSQTVSSGATNGAESKT 2544 KESESTTTSSESSKPSQDEN 2679 TPPVIDSVSEKANPNIKDSK 2604 SPKSL - VKSTTSPSTVTSS 2733 QKGTEIKPGQNNPVPVSETN 2662 ESTTESSEAPTTPAKTSETK

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RyTettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heide non, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapple, F. non, T.; Hocky, E.K.; Holt, I.S.; Mith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A;Title: Complete Genome Sequence of a virulent isolate of Streptococcus pneumoniae.
A;Reference number: A95000; MUD:21357209; PMID:11463916
A;Status: preliminary
A;Rolecule type: DNA
A;Residues: 1-4776 KMR>
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                                                                                                                                                                                                                                                                                                                                                                                cell wall surface anchor family protein [imported] - Streptococcus pneumoniae (strain TIC C.Species: Streptococcus pneumoniae C.Species: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001 C.Accession: E95206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          45;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            622
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            671 SHSLTIVSNACGTLWNLSARNP-----KDQEALW---DMGAVSMLKNLIHSKHKMI
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                                                                            2709 STMSSTSSEPETNAPAVTVSSEA--SSTTLEENSSTSSPTSSEASVKLSSL 2757
     2793 SSADSTSARPSQIPTPVNNNTKKRDSKTDSTESSGTQSPKRHSGSYLVTSV 2843
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels 342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 4776;
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Cispecies: Homo sapiens (man)
Cibate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
Cibate: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 05-Nov-1999
Cibates solution: Bruce, D.; Mundt, M.; Doggett, N.; Munk, C.; Saunders, E.; Robinson, re, J.; White, S.; Ueng, S.; Tatum, O.; Campbell, C.; Fawcett, J.; Deaven, L. submitted to the EMBL Data Library, March 1998
A;Description: Sequencing of human chromosome 16p13.3.
A;Reference number: Z14664
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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residuces: 1-1791 <RIC>
A;Cross_references: EMBL:AC004493; NID:g2996648; PIDN:AAC08453.1; PID:g2996650
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A; Introns: 1610/2; 1706/2
A; Note: KIAA0324
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es 744; Indels	-TPSSNAKRQNQLHPSSAQSRSGQPQKAATCKVSS	:		- - OBKSKDSLVQSCPGSLSLCAGVKSTPPGESYFGVSSLQLKGQSQTSPDHRSDTSSPEV	KEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPS	-HSESPSLQSKSQTSPKGGRSRSSSPVTĒLĀSRSPIRQDRGEFSASPML	KSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGWVSGIISP	SDSSSYPTVDSNSLLGQSRLËTAESKEKMALPPQE	MPPSRSKTPPPPPQTAQTKREVPKOKAPTAEKRESGPKQAAVN	ESTADORSC SST.S STSSS SST STATE	RPA	-PVQENDNGNETESEQPKESNENQEKEAF	: : : : : :	KIIDSEKDLIDDSDDDDIEILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPV	RSSGHSSSELSPDAVEKAG	H	KSSSASSPEMKDGLI	EGVRGGAGSGEFEKKUTIPIEGRSTDEAQGGKISSVIIPELDDNKAEEGDILAECTNS	Ġ	: : :	V RKNADSKONLINAERV FSDNKDSKKONLKONSKDFNDKL, PINNEDR VRGSFAFDSPHHY	: ::: : SDSSPDSKAKTR	TPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQS	-SKSRLSPRRSRSGSSPEVKDKPRAAPRAQS	ANKTQAIAKQPINRGQPKPILQKQSTFBQSSKDIPDRGAATDEKLQNFAIENTPVCF	RRŚRSGSŚŚKGRGPSPEGSSSTES	SHNSSLSSLSDIDQENNNKENEP-IKETEPPDSQGEPSKPQASGYAPKSFHVED	KSRTARRGSRSSPEPKTKSRTPPRRRSSRSSPELTRKARLSRRSRSASSPE	TPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKRPSFLKGDNEKHSPRNMGGIL	SASSPRTKTTSR-RGRSPS	GEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQBGANSIVSSLHQAAAAACLGRQASSDS SRSRREKTRTTRREDROGSOSTERRROBERRE	DSILSLKSGISLGSPFH-LTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGG	
e 251; Mismatches	ANSSAL	: TPPRQSHSGSISPYPKV	1255 NQETIQTYCVEDTPICFSRCSSL-SSLSSAEDEIGCN	GSLSLCAGVKSSTPPGE	EVPAVSQHPRTKSSR	ESPSLOSKSOTSPKGGR	VQETPLMFSRCTSVSSL		1 0000	OLD OLD OLD OLD OLD OLD OLD OLD OLD OLD	 SEEPAGQILSHLSSELKI	Q	 WGGPHFSPEHKELSNSP]	ODDIELLEECTISAMPTI	IDPSLDMKEQSTRSS	RLOPOKHVSFTPGDDMPRVYCVEGTP	SISSPVLDAVPRTPSRE	SKKDIIPIEGRSTDEAQGGKI : : : : : : : : : : : : : : : : : : :	KIMDQVQQASASSAPNI	: : RPRSRSPSSPEI	AERVFSDNKDSKKONLKO	: : : /KPSASPQERSE	SLSSLDFDDDDVDLSREP	-QRSRSGSSPEVDSF	SQPKPILQKQSTFPQSSK 		SNNNKENEP-IKETEPPI :	gersspepktrksrtpp	SSLSIDSEDDLLQECIS	/SSPEPAEKSRSSRRRRS	SEHGLSPDSENFDWKAI	PH-LIPDQEEKPFISNK	SRVTRRRRGGSGYHSRSPARQESSRTSSRRR
382; Conservative	HMSSSSENTS	: 1 HSGSSSPDTKVKPE	NOETIQIYCVEDIP		KEKIGTRSAED	RQS) KSG~MSPEQSRFQ	DLPDSPGQT 	AAVORVOVL		KDVELRIMP			VKEDLNGPFLNQLETDPSLDMKE								TPLR		GSDSSPEPKAPAPKALP							
Matches 38	Qy 1210	Db 1	Qy 1255	Db 50	Qy 1308	109		Db 160	Oy 1422	,		Qy 1518	Db 323	Qy 1555	Db 383	Qy 1615		UY 16/3	Н	Db 516	Qy 1.789	Db 565	Qy 1847	Db 603	Qy 1907	Db 649	Qy 1964	969 qa	7	DD 748	Qy 2073 Db 807	Qy 2133	DD 840

RESULT 14

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147; 226 245 298 580 166 156 124 WYYAQL-QNLTKRID-----SLPLTENFSLQTDMTRRQLEYEAR-----QIRVA 199 SPRVGKIWTERWRGGMVPVQTSTETARMKTPVRHSQQLKDEDSRV-----TGRRH 337 SAPRRL---TSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLLAMSSSQDSCISMRQSGCLPL 355 LSSVDISNFGDSI--NKSEGMPMKRRRVSFGGHLRPELFDENLPPNTP-LKRGETPTKRK 498 ELGGLQAIAELLQVDCEMYGLINDHYSITLRRYAGMALINLIFGDVANKATLC-SMKGCM 526 583 634 611 694 651 | : | : | : | STANDYEKQQQ----MSDTGSVLSNSANLSERQLQVTNSGDIPEPITTEILGEKV 750 --HRQILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSAR 690 LSSTRNAAKQQSDRYSASPTLRRRSIKHENTVQT---PKNVHNIT------DLEKK 797 QVQDNENAPQRCKESGELSEGSEKTSARRSSARKQKPTKDLIGSQMVTQTADYAEELLSQ 917 ASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSSRGSLD 842 SVNLDEGGSAQAVHKTVTPG----KLATRNQTPVEAGDVGSPADTPEH-----SSSPQR 387 LIQLIHGNDKDSVLLGNSRGSKEARARASAALH-----NIIHSQPDDKRGRREIRVL 407 HILEQIRAYCETCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMN 467 731 TPVSETEPLKTASSVSKLRRSRELRHTLVETMNEKTEAVLAENTJARHLRGTFREOKVDQ 857 -----NRPAKYKDANIMSPGSSLPSLH---VRKQKALEAELDAQHLSETFDNIDNLSPK 782 A;Cross-references: EMBL:X82786; NID:g1177527; PIDN:CAA58026.1; PID:g1177528
A;Experimental source: strain CBA; testis
C;Genetics:
A;Gene: Ki-67
C;Keywords: cell cycle control; nucleus; tandem repeat : |::|:|::|: GSKNSVSQDSSGHVEQHTGRNIVEPTSGGSLLRSPGLQGAVTGNRSLLPTQSLSNSNEKE TPKKPTSNLHNQFTTGHANSPCTIVVGRAQIEKVSVPARPYKMLNNLMLNRKVDFSEDLS TEFPGKSLGKEPSRRA--SRDSFCADPDGEGQDTKASKWTASRRSFVYAKGLSADSPASD MEEQLG------TCQDMEKRAQRR--IARIQQIEKDILRIRQLLQSQATEAERS SONKHETGSHDAERONEGOGVGEINMAT ----SGNGQGSTTRMDHETASVLSSSSTH 499 SLGTHSPAVLKTIIK-ERPQSPGKQESPGIIPPRIN-------DQRRRSGRT SSG-----SNFLCETDIPKKAGRKSGNLP----AKRASISRSQHGIL RALVAQLKSESEDLQQVIASVLRNLSWRADV---NSKKTLREVGSVKALMECALEVKKES ---ENKADICAVDG NP-KDQEALWDMGAVSMLKNLIHSKHKMI------AMGSAAALRNLMA-----G-----QGTIQNL-----EESWHMQNTSISEDQG---ITEKKVNIIVYATKEKHSPKTP Gaps 932; SNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSF--PRRGFV----2.9%; Score 420; DB 2; Length 2938; 18.6%; Pred. No. 3.3e-09; live 439; Mismatches 1268; Indels 93 ALAFLVGTLTYRSOTNTLAIIESGGGILRNVSSL-----IATNED-TLKSVLSALWN-----LSAHCT--Conservative 439; Best Local Similarity Matches 604; Conserv 80 200 338 388 408 584 612 751 798 157 287 695 Query Match 227 246 299 356 543 527 581 635 652 691 732 В ò d 엄청 g oy Oy 8 & B & à ઠે ò qq δ d ò g & A 8 8 g Q Dp 정 8

LGKSKKKAQPLEDLTCFQELFISPVPTNIIKKIPSKSPHTQPVRTPASTKRLSKTGLSKV 1138 1466 QPGFVR-TPRTSKRLAK-TSVGNIAVREKISPVSLPQCATGEVVHIPIGPEDDTBNKGVK 1523 1479 VQVLPDADTLLHPATESTPDGFSCSSSLSALSLDEPFIQKDVELR-----IMPPVQENDN 1533 1582 ALQSPQPGHIINPASMKRQSNMSLRKDMREFSI----LEKQTQSRGRDAGTPAPMQE-EN 1636 1637 GTTAIMETPKQKLDFIGNSTGHKRRPRTPKNRAQPLEDLDGFQELFQTPAGASDPVSVEE 1696 1577 ECIIS-----AMPTKSSRKAKKPAQTA-SKLPPPVARKPSQLPVYKLLPSQNRLQPQKHV 1630 : : | : : | : : | | | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 982 SIBSYSEDDESKFCSYGOYPADLAHKIHS-----ANHWDDND--GELDTPINYSLKY 1031 BEQHEBEERPTNYSIKYNEEKRHVDQPIDYSLKYATDIPSSQKQSFSFSKSSGGSSKTF 1209 DSPGQIMPPSRSKIPPPPPPPQIAQIKREVPKNKAPIAEKRE-----SGPKQAAVNAAVQR 1478 SFTPGDDMPRVYCVEGTPI----NFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFE 1685 ----GKRMKSLGRAPGTPAPVQEENDSTA-----FMETPKQKLDF-----TGNSSGHKR 1781 MPK-GKSHKPFRVKKIMDQVQQASASSAP------NKNQLD-----GKKKK 1771 KKV-DMKEESSALTKRIHMPGESRHNPKILKLEC--EDIKALKQSENEMLTSTVNGSKRT 1178 -KQKLESIENLTGLRKQSRTPKDITGFQD9FQIPDHANG------PLVVVKT--KKAMFF HMSSSSENTSTP----SSNAKRQNQLHPSSAQSRSGQPQKAATCKVSSINQET KDRSLERER-GIGLGNYHPATENPGTSSKRGLQISTTA LPKIILRKMDV----TEBISGL--WKQSLGRVHTTQEQEDNAIKAIMEIPKETLQTAADG 1416 TRLTRQP------QTPKEKVQPLEDHSVFQE--LFQTSRYCSDPLIGNKQTRMSLRSP IQTYCVEDTPICFSRCSSLSSLSSAEDEIGCNQTTQEADSANTLQIAEI-KEKI-----G KRDTIPTEGRSTDEAQG-----GKTSSVTIPE----LDDNKAEEGDILAECINSA 885 AQIAKVMEEVSA----IHTSQEDRSSGSTTELHCVTDERNALRRS-----SAAHTHSNT YNFTKSEN---SNRTC----SMP---YAKLEYKRSSNDSINSVSSSDGYGKRGQMKP 1032 SDEQLNSGRQSPSQNERWARPKHI--IEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKF QPHFGQQECVSPYRSRGANGSETNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSE EEHLQLGEGVDTFQVSTNKVIRSSRKPAKRKLDSTAGMPNSKRMRC----SSKDNTPCLE TRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSP 1373 PEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPC-SGMVSGI-ISPSD----LP ESTPOTLDSSASRTVSKROOGAHEER--POFSGDLFHPOELFOTPASGKDPVTVDETTKI GNETESEQPKE----SNENQEKEAEKTIDSEKDLLDDSD------DDDIEILE SAKISLASSQAEPVRTPASTKRRSKTGLSKV--DVRQEPSTL---DLNGFQELFQMPGYANDSLTTGISTMLARSPQLGPVRTQ-SSESE-843 1022 1228 1210 1318 1362 1524 1150 1425 1259 1631 1737 1313 g 6 6 6 6 8 6 8 6 8 6 8 6 8 6 8 6 8 8 8 8 8 & 8 & 8 8

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g v		2867
<u>م</u> م	1874 LSREKABLRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINRGQPKPILGKQS 1931 	Oy 2818 SKT 2820 SKT 2820 Db 2919 AKT 2921
οy	1932 TFPQSSKDIPDRGAATDEKLQNPAIENTPVCFSHNSSLSSLSDIDQENNNK 1982	RESULT 15
qq	2059 ISLESSQAEPVRTRASTKRLSKTGLNKYDVREGH-SPLSKSSCASQKVMQTLTLGEDHGR 2117	hypothetical protein Fig. C.Species: Caenorhabdi
ζ. O.	1983 EN	C, Date: 15-Oct-1999 #85 C, Accession: T20532; T R; Palmer, S.
Š	TPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKFSRLKGDNEKHSPRNMGGILGEDL	submitted to the EMBL A;Reference number: Z1
Dp		A; Accession: T20532 A; Status: preliminary;
ò	TLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSIL	A;Residues: 1-2722 <wii A;Cross-references: EMI</wii
qq	EPEGEGKVIKTRKQSVKRKLDTEVNVPRSKRQRITRAEKTL	A;Experimental source: R;Gajadsty, S.
λo	SLKSGISLGSPFHLTPDQEEKPFTSNKGPRILK	submitted to the EMBL A;Reference number: Z2
pp		A; Accession: T27777 A; Status: preliminary;
δ	2170 PGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSBISGQMKQPLQANMPSI 2224	A;Molecule type: DNA A;Residues: 1-2722 <wi< td=""></wi<>
Db	2332 ÞORKTÍRVVROÍRNTOKÉPISDNQÉMEEFKESSVOKÓDPSVSLTÉRRNÓPRIVKEKTOPL 2391	A; Cross-references: EM A: Experimental source:
D Q	2225 SRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPS-EG 2264 2392 BELTSFQEETAKRISSKSPQPEEKETLAGLKRQLRIQLINDGVKEEPTAQRKQPSRET 2449	C,Genetics: A,Gene: CESP:F07All.6b A,Map position: 2
à	2265 QTATISPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQ 2314	A; Introns: 36/2; 92/2;
Db	2450 RNTLKEPVGDSINVEEVKKSTKQKIDPVASVPVSKRPRRVPKEKAQALE 2498	Query March Best Local Similarity Matches 460: Conse
δλ	2315 -QPLSRPIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKM-SYTSPG 2370	OV 811 SDNFNTGN
Db	2499 LAGLKGPIQTLĠHTDEŚASDKĠPTQMPCNSLQPEQVDŚPQŠSPRRPRTRRĠKVEADBEPS 2558	357
Š	2371 ROMSOONLTKOTGLSKNASSIPRSESASKGLNOMNGNGANK-KVELSRMSSTKSSGSES 2429	17.6
Db	2559 AVRKTVSTSRQIMRSRKVPEIGNNGTQVSKASIKQTLDTVAKVTGS 2604	, 60 , 60 , 60 , 60
οy	2430 DRSERPVLVRQSTFIKBAPSPTLRRKLBESASFESLSPSSRPASPTRSQAQTPVLSPSLP 2489	928
Db	2605krolrthkcwgstilkkilgdskbitoisdhsb 2636	:: : DD 444 SNEDSDEO
ò	2490 DMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKR 2549	886
Db	2637KLAHDTSILKSTQQQKPDSVKPLRTCRRVLRASKBVPKEVLVDTR 2681	494
č	2550 EHSK-HSSSIPRVSTWRRTGSSSSILSASSESSEKAKSEDE 2589	1043
QQ	2682 DHATLQSKSNPLLSPKRKSARDGSİVRTRALRSLAPKQEATDEKPVPEKKRAASSKRYVS 2741	535
ζ	2590KHVNSISGTKOSKENQVSAKGTWRKIKENEFSPINSTSQTVSSGAINGAESKTL 2643	1096
d d	2742 PEPVRMKHLKIVSNKLESVEGOVSTVMKTEEMEAKRENPVTPDQNSRYRKKTN 2794	Db 589VSSF-
<i>\delta</i>	2644 IYQMAPAV-SKTEDVWYRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQA 2702	Qy 1140 PINYSERY
9 8	PGONNPVPVSRTNESSIVERTPF	DD 637 PRDYYY
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Table 1919 ART 2911 BESULT 15 TO 2019 ART 2911 BESULT 15 TO 2019 ART 2911 BESULT 15 TO 2019 ART 2911 BESULT 15 TO 2019 ART 2911 BESULT 15 TO 2019 ART 2911 BESULT 15 TO 2019 ART 2911 TO 2019 ART 2911 BESULT 15 TO 2019 ART 2911 TO 2	Hext_change 29-Oct-1999
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qu	1607	
ολ	2114`	SLHQAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPT 2160
qq	1652	GDEDSV
ò	2161	2172 SNKGPRILKPGE 2172
Db	1704	QSIFDEEEADEFPQYPDFGISTNEKEVSGKDPHNIKPTEPLNNGHTDLLFSPSSSAHASE 1763
Qy	2173	-KSTLETKKIESESKGIKGGKKV-YKSLITGKVRSNSEISGQWKQ 2215
Db	1764	
οy	.2216	SSSTSPVSKKGPP
Ор	1824	MEESPEGTPTPDLISNNESQDTPGAVNNHLHENHDAVQTPIQLQPASQHQVAQPS 1878
È	2271	PRGAKPSVKGELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSIS 2330
QD	1879	PRPAVAPDSQQNGPVLVSQQSQPSPMSSQQSDMAQNLIL 1917
ζō	2331	PST
qq	1918	SSKDINDLAAKLHKNPEALAQATRGDCSGIFQHLLLHAQGNGQNMTPEMLQLKAAFF 1974
ò	2391	IPRSESASKGLNOMN NGNGANKKVELSRMSSTKSSGSESDRSER 2434
qq	1975	AQQGNEANQMMQAKMKQQTINKDRIKEQERVKRMYBENBRKVEEDBREKQRKEEBRQRL 2034
ζ	2435	PVLVROSTFIKEAPSPTLRRKLE 2466
qq	2035	
δ	2467	PTRSQAQTPVLSPSLPDMS
qa	2095	ATNGVLHLPTQSIQRPSS-TASTSSNPPKAPLQPSASVNQNTIDPAEIEEIRVQRWFYKP 2153
8	2509	PNLSPIIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTW 2564
qq	2154	LKMSAEEAATVMAVASSDRNPPATSTVDLAAMLQQLQAAQAAQAAQQVPVVTTA 2207
ò	2565	RRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSP 2622
qq	2208	STPNPLSNLETLSTASLANLATGGALNPLSMLALTSSLNGSSPVYGGIARVLITMNMGQ 2267
ò	2623	TNSTSQTVSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGN 2678
qq	2268	MLATHQTSELLATMN-QQETLMALLAARNGLPFAMPQQNQQPQMPAQGG 2315
ò	2679	TPPVIDSVSEKANPNIKDSKONQAKQNVGNGSVPMRTVGLENRINSFIQVDAPDQKGT 2736
QQ	2316	FAIPTVLPHMSLKRNAKDQLSVGGVSDRKKSCPLHAMIGQGQQPPPPQQPMQ 2367
ò	2737	EIKPG2NNPVPVSETNESSIVER
qu	2368	. AVAPAPPRSPSPPRKSMFENLPPEMKEKNEMPRKEILRRLDIILLEBLGÅEDEBDQKPDL 2427
à	2760	TPFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVNNNTKKRDSK 2819
Db	2428	KQIPTSEEDTDDSKADSMGAEGSAFRRILS-RSSTWGNNSGSPSASGTTSPS 2478
δλ	2820	TDSTESSGTQSP 2831
Dp	2479	TSSSISSGPDSF 2490
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Search completed: August 25, 2004, 17:25:21 Job time: 96 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

August 25, 2004, 16:58:21; Search time 32.5 Seconds (without alignments) 4554.937 Million cell updates/sec Run on:

Title: Perfect score: Sequence:

US-09-442-489F-7 14566 1 MAAASYDQLLKQVEALKWEN........ESSGTQSPKRHSGSYLVTSV 2843

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

141681 segs, 52070155 residues Searched:

141681 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_42:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SOMMAN	th DB ID Description	1 APC HUMAN	1 APC_RAT P70478 rattu	MOUSE Q61315 mus	1 MAPA RAT P34926	1 SPEN_DROME	1 MINT HUMAN Q96t58 homo	1 MINT_MOUSE Q62504 mus 1	1 ZEP1 MOUSE Q03172 mus	1 MAPA HUMAN	1 ANK2 HUMAN Q01484 homo	1 PGCV_CHICK Q90953 gall	1 PCLO RAT Q9jks6	1 PCLO_HUMAN	1 MLL3 HUMAN Q8nez4	1 CENF_HUMAN P49454	1 MAPB_RAT P15205	1 ANK3_HUMAN Q12955	1 KI67_HUMAN P46013	1 PCLO_CHICK Q9pu36 gallu	1 PPRB_HUMAN Q15648	1 HRX HUMAN Q03164	1 NCRI_MOUSE Q60974 mus m	1 TCOF_HUMAN Q13428 homo	1 NCR1_HUMAN 075376 homo	1 MAPB HUMAN P46821 homo	1 GOB1_HUMAN	1 CENE HUMAN Q02224 homo	1 ATRX_PANTR Q7ygm4 pan t	1 BPA1 MOUSE Q91zu6 mus	1 PCLO_MOUSE Q9qyx7 mus	1 UN89_CAEEL 001761 caen	
dk	Query Match Length		90.6	ī.	٤.	۳.	٦.	σ.	ω.	ω.	٠.	۲.	۲.	.7	७.	9.	φ.	9.	9.	9.	φ.	ıv.	ĸ.	'n.	r,	ĸ.	s.	rύ	'n.	5.	s.	2.5	
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ALIGNMENTS

RESULT 1 APC_HUMAN APC_HUMAN AC P25054; Q15162; Q15163; DT O1-MAY-1992 (Rel. 22, Created) DT O1-MAY-1992 (Rel. 22, Last sequence update) DT O1-MAY-1992 (Rel. 23, Last annotation update) DE Adenomatous polyposis coli protein (APC protein). DE Adenomatous polyposis coli protein (APC protein). SO Homo sapiens (Human). SO Homo sapiens (Human). CO RIMALYCAI, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; CO Mammalia; Eutheria: Prinates; Cararrhin; Hominidae: Homo.	rimates; Catallinn; Hominicae; ubMed=1651562; T. Preisinger A.C., Hedge P., Mc; M.A. Groffen J., Boguski M.S., Al Miyoshi Y., Miki Y., Nishisho I., FAP locus genes from chromosome 56 (1991).		MEDLINE-95174643; Pubmed-7661930; Hamilton S.R., Liu B., Parsons R.E., Papadopoulos N., Jen J., Powell S.M., Krush A.J., Berk T., Cohen Z., Tetu B., Burger P.C., Powell S.M., Taqi F., Booker S.V., Petersen G.M., Offerhaus G.J.A., Tersmette A.C., Giardiello F.M., Vogelstein B., Kinzler K.W.; The molecular basis of Turcot's syndrome."; WWW Engl. J. Med. 332:839-847(1995). [5] DISEASE. DISEASE. Eccles D.M., van der Luijt R.B., Breukel C., Bullman H., Bunyan D., Fisher A., Barber J., du Boulay C., Primrose J., Burn J., Fodde R.; "Hereditary desmoid disease due to a frameshift mutation at codon 1924 of the APC gene.";
RESULT APC HU ID A DT O DT	RAR RAR RAR RAR RAR RAR RAR RAR RAR RAR	R R R R R R R R R R R R R R R R R R R	RY RA RY RY RY RY RY RY RY RY RY RY RY RY RY

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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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STRAIN=FRECHER 344/N; TISSUE=Brain;
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16-OCT-2001 (Rel. 40, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Adenomatous polyposis coli protein (APC protein)
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and Fischer 344/N;
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Interpro; IPR000225; Armadillo.
Ffam; PR00514; Armadillo_seg; 4.
SWART; SW00185; ARM; 5.
FROSITE; PS50176; ARM REPEAT; 1.
Wht signaling pathway; Anti-oncoge
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STRAIN-Sprague-Dawley, and Fisch
MEDLINE-95148647; PubMed=7846077
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axin (By similarity).
ALTERNATIVE PRODUCTS:
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                SSESSEKAKSEDEKHVNSISGTKQSKENQVSAKGTWRKIKENEFSPINSTSQTVSSGATN 2636
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"APC gene messenger KNA: novel isoforms that lack exon 7.";
Cancer Res. 53:5589-5591 (1993).
-!- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTINNB1 and participates in Wnt signaling. APC activity is correlated with its phosphorylation state (By similarity).
-!- SUBUNIT: Forms homooligomers. Associates with catenins. Binds
                                                                                                                                                                             GAESKTLIYQMAPAVSRTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSISEKGNPSIKD
                                                                                                                                                                                                                             2756 AERTPFSSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTSARPSQIPTPVGSSTKKR
    EESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIE
                                                                                               2637 GAESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKD
                                           2517 YNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVSTWRRTGSSSSILSA
                                                                                                                                                                   SKDNOAKQNVGNGSVPMRTVGLENRLNSFIQVDAPDQKGTEIKPGQNNPVPVSETNESSI
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                                                                                                                                                                                                                                                                                                                                                                                                                                              SECURNCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.
STRAIN=CS7BL/6J, and CAST/BI; TISSUE=Brain;
MEDINES=22631011, PubMed=1150108.
Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R., Luongo C., Gould K.A., Dove W.F.;
Multiple intestinal neoplasia caused by a mutation in the murine homolog of the APC gene.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R. Luongo C., Gould K.A., Dove W.F.; Science 256:1114-1114(1992).
                                                                                                                                                                                                                                                                                                                                                                                                           Bukaryota, Metazoa; Chordata, Craniata; Vertebrata, Buteleostomi,
Mammalia; Butheria; Rodentia; Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                          Vertebrata; Euteleostomi;
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Dicker F., Lambertz S., Reitmair A., Ballhausen W.G.;
"The murine APC gene: alternative splicing of 5' untranslated
                                                                                                                                                                                                                                                                                                                         APC MOUSE STANDARD; PRT; 2845 AA.
Q61315; Q62044;
16-0CT-2001 (Rel. 40, Last sequence update)
10-0CT-2003 (Rel. 42, Last annotation update)
Adenomatous polyposis coli protein (APC protein) (mAPC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases
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MEDLINE=94061824; PubMed=8242607;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its way mon-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                        Isoid-061315-4; Sequence=VSP 004116, VSP 004117; TISSUE SPECIFICITY: Expressed in liver, spleen, kidney, heart, lung, brain, stomach, intestine, testis and ovary. PIM: Phosphorylated by GSK3B (By similarity). SIMILARITY: Contains 7 ARM repeats:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Missing (in isoform 2 and isoform 4). /FIId=VSP_004116.
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GO; GO:0005737; C:Cytoplasm; IDA.
GO; GO:0005737; C:Cytoplasm; IDA.
GO; GO:0005633; F:beta-catenin binding; IDA.
GO; GO:000952; P:anterior/posterior pattern formation; IMP.
GO; GO:000959; P:axis specification; IMP.
GO; GO:000959; P:dorsal/ventral pattern formation; IMP.
GO; GO:0016055; P:Wnt receptor signaling pathway; IDA.
InterPro; IPR008938; ARM.
InterPro; IPR008255; Armadillo.
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COLLED COIL (POTENTIAL)
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ASP/GLU-RICH (ACIDIC) .
ASP/GLU-RICH (ACIDIC) .
Event=Alternative splicing; Named isoforms=4;
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                                                                                                 Sequence=VSP_004116;
                                                                                                                                                   IsoId=Q61315-3; Sequence=VSP_004117;
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                                                 IsoId=Q61315-1; Sequence=Displayed;
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Pfam; PF00514; Armadillo_seg; 4.
SMART; SM00185; ARM; 5.
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Wht signaling pathway; Anti-onco
Alternative splicing; Repeat; Co
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EMBL, U02937, AAA03443.1; -.
PIR, I49505, I49505.
HSSP, Q02248; 3BCT.
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KPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGOMKQP
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi, Muridae, Murinae; Rattus.
NCBI_TaxID=10116;
                KPFTSNKGPRILKPGEKSTLEAKKIESENKGIKGCKKVYKSLITGKIRSNSEISSQMKQP
                                                         LOANMPSISRGRIMIHIPGVRNSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKP
                                                                                                                   SVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSRPIQSPGRNSISPGRNGI
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J. Biol. Chem. 267:16561-16566(1992).
-!- FUNCTION: Structural protein involved in the filamentous cross-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Brain;
MISPLINE-29355629; PubMed=1379599;
MISPLINE-29355629; All Misser C.C.
MISPLINE-3935629; All Misser C.C.
MISTOCLUBULE-associated proteins 1A and LC2. Two proteins encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-FCB-2001 (Rel. 40, Last annotation update)
Microcumbule-associated protein 1A (MAP lA) [Co
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long a sits content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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bridging between microtubules and other skeletal elements.
SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAPIA and MAPIB proteins.
TISSUE SPECIFICITY: BRAIN, HEART AND MUSCLE.
DEVELOPMENTAL STRGE: EXPRESSED LATE DURING NEURONAL DEVELOPMENT APPEARING WHEN AXONS AND DENDRITES BEGIN TO SOLIDIFY AND STABILIZE
                                                                                                                                                                                     THEIR MORPHOLOGY.

-1- DOWALN: THE basic region containing the repeats may be responsible for the binding of MAPIA to microtubules.
-1- PTM: LC2 the binding of MAPIA to microtubules.
-1- PTM: LC2 IS CORRERESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FROM MAPIA BY PROTECLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH BOTH MAPIA AND MAPIB.
-1- SIMILARITY: TO MAPIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           90 IGADNIPGINGLLQRK------VAELEEGSGGSSSSYSDWVKNLISPELGVVFFNVPD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VLÁPVKDSKEMQFLMQKWAGNSKAKTGIVLANGKEAEISVPYLISITALVVWLPANPTEK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       701 MGAVSM--LKOLIHSKHKMIAMGSAAALRNLMANRPAKYKD--ANIMSPGSSLPSLHV--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ------RKQKALEAELDAQHLSETFDNIDNLSPKASHRSKQR---HKQSLYGDYVF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 KLRLPDASRKAKRSIEEACLTLQHLNRLGIQAEPLYRVVSNTIEPLTLFHKMGVGRLDMY
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1. Phosphorylation.

2774 MAP1 LIGHT CHAIN LLs.

2774 LYS-RICH (BASIC).

11 X 3 AA REPEATS OF K-K-[DE].
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.3%; Score 476; DB 1;
18.6%; Pred. No. 3.2e-10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              entities requires a license agreement (S
or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; M83196; AAB48069.1; -. PIR; A43389; A43389; M40crotubule; Repeat; Phosphor CHAIN 72465 2774
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MEDLINE=20196006; PubMed=10731132;
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                                                                                                                                                                                                2559 GLSSESGRVERLIREXGRPGRRAPGRAXPASPARRLDIR---GKRSPTPGKGPVDRTSRTV 2615
| | | | : | | : | | : | | : | | 2324 PFLSPSGD--HEANGPGETSLNPDGFVTATAEKEEAEAPHAWERGSWPEGAERSSRPDTL 2381
                                                                                                                                   2748
                                                                                                                                                  2749 SETNESSIVERIPPS-----SSSSSKHSSPSGTVAARVTPFNYNPSPRKSSADSTS---
                                                            2382 LSSEQPLRPGKSSGGPPCSLSSEVEAGPQGCATDPRPHCGELSPSFLNPPLPPSTDDSDL
                                                                                    2660 RIEDCPI----NNPRSGR-SPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGSVPMR
                                                                                                           2442 STEEARLAGKGGRRRVGRPGATGGPCPMAD---ETPPTSASDSGSSQSDSDVPPETEECP
                                                                                                                                     2715 TVGLENRLNS-----FIQVD-APDQKGT-EIKPGQNNPV-----------PV
                                     --APAVSKTEDVWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. (ISOFORMS 3 AND 4), FUNCTION, ALTERNATIVE PROMOTER USAGE, TISSUE SPECIFICITY, DEVELOPMENTAL STAGE, AND MUTANTS B9 AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rebay I., Chen F., Heiso F., Kolddziej P.A., Kuang B.H., Laverty T., Suh C., Voas M., Williams A., Rubin G.M.;
"A genetic screen for novel components of the Ras/mitogen-activated protein kinase signaling pathway that interact with the yan gene of Drosophila identifies split ends, a new RNA recognition motif-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-20025936; PubMed=10556062;
Wiejlette E.L., Harding K.W., Mace K.A., Ronshaugen M.R., Wang F.Y.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "spen encodes an RNP motif protein that interacts with Hox pathways to repress the development of head-like sclerites in the Drosophila
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=20171275; PubMed=10704397;
Klang B.H., Wu S.C.-Y., Shin Y.-A., Luo L., Kolodziej P.A.;
"split ends encodes large nuclear proteins that regulate neuronal
cell fate and axon extension in the Drosophila embryo.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. (ISOFORM 1), SUBCELLULAR LOCATION, AND TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa, Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                     SPEN_DROME STANDARD; PRT; 5560 AA. QBSX83; Q9WEL1; Q9WEL2; L10-OCT-2003 (Rel. 42, Tested) 10-OCT-2003 (Rel. 42, Last sequence update) 10-OCT-2003 (Rel. 42, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND TISSUE SPECIFICITY. STRAIN=Berkeley;
                                                                                                                                                                                                                                                                                                                                                                                                         Drosophila melanogaster (Fruit fly)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Embryo;
MEDLINE=20157049; PubMed=10655223;
                                     2625 -STSQTVSSGATNGAESKTLIYQM-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Development 126:5373-5385(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM 4).
                                                                                                                                                                                                                                   2800 ARPSQIPTPVNNNTKK 2815
                                                                                                                                                                                                                                                          2616 PRPRSTPSOVTSAEEK 2631
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Senetics 154:695-712(2000)
                                                                                                                                                                                                                                                                                                                                                                                 Split ends protein.
SPEN OR CG18497.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Embryo;
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RA MEDILAREZOLOGOS, TOTALEZONOS, TOTALEZONOS, TOTALEZONOS, TOTALEZONOS, SCHERE S.E., Totalede P.G., Scherer S.E., It'P FW., Hoskins R.A., Galle R.F., Statementides P.G., Scherer S.E., It'P FW., Hoskins R.A., Galle R.F., Statemen G.G., Scherer S.E., It'P FW., Hoskins R.A., Galle R.F., Statemen G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X., S.W., Statemen J.R., Barach R.G., Champen M., Pfeifer E.D., RA Abril J.F., Abadrawa P.C., Champen M., Pfeifer E.D., Ballew R.M., Bagan A., An H.-G., Blaze's F.G., Champen M., Pfeifer E.D., Ballew R.M., Bagan A., An H.-G., Blaze's F.G., Champen M., Doyle C., Barker, E.G., Helt G., Nelson C.R., Miklos G.L.G., Baldwin D., Ballew R.M., Bagan A., An H.-G., Blaze's F.G., Champen M., Bessley E.M., Ballew R.M., Bagan A., An H.-G., Blaze's F.G., Champen M., Barker S.A., Dallek C., Bayraktaroglu L., Beasley E.M., Ballew R.M., Band D.A., Buller H., Cadieu E., Center A., Chandra I., Bartis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I., Backer J.M., Band D.A., Buller H., Gadieu E., Center A., Chandra I., Backer J.M., Doyle C., Gabriellan A.E., Davies P., Ander B.D., Ballek C., Davenport L.B., Davies P., Ander B.D., Ballek C., Davenport L.B., Davies P., Ander B.B., Contrell J.H., Gu Z., Ferriag S., Dulkov B.C., Dunn P., Ballek A., Gong F., Gorrell J.H., Gu Z., Ferriag S., Fleischmann W., Rosler C., Gabriellan A.E., Garg N.S., Gabrat W.M., Glasser K., Harris N.L., Harvey D.A., Henman T.J., Wei M.-H., Ibeywam C., Alandra F., Karpen G.H., Ke Z., Kemison J.B., Natien B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Harkey D.A., Helman T.G., Morsis C., Morsis D.M., Natien B. B., Nollhor K.A., Howley B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Murphy B., Mur
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STRAIN-Berkeley, TISSUE-Embryo;
MEDLINE-22426066; PubMed=12537569;
Stapleton M., Carlson J.W., Brokstein P., Yu C., Champe M.,
George R.A., Guarin H., Kronmiller B., Pacleb J.M., Park S., Wan K.H.,
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REVISIONS, AND ALTERNATIVE SPLICING.
MEDLINE=22426069; PubMed=1257572;
Migra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
Smith C.D., Tupy J.L., Whitfield B.J., Bayraktarogul L., Berman B.P.,
Smith C.D., Tupy J.L., Whitfield B.J., Sayraktarogul L., Berman B.P.,
Bettencourt B.R., Celniker S.E., de Grey A.D.N.J., Drysdale R.A.,
Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Annotation of the Drosophila melanogaster euchromatic genome: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genome Biol. 3:RESEARCH0083.1-RESEARCH0083.22(2002).
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"A Drosophila full-length cDNA resource.";
Genome Biol. 3:RESEARCH0080.1-RESEARCH0080.8(2002).
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MEDLINE=20414403; PubMed=10959845;
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Science 287:2185-2195(2000).
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PROSITE; PS50917; SPOC; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Name=3: Synonyme=Speni;
Isold=Q8SX83-3; Sequence=VSP 008567;
Note=Produced by alternative pplicing of isoform 1;
Name=4; Synonyme=Spenis;
Isold=Q8SX83-4; Sequence=VSP 008565, VSP 008566, VSP 008567;
Note=Produced by alternative pplicing of isoform 2;
Note=Produced by alternative pplicing of isoform 2;
Isold=Q8SX83-4; Sequence=VSP 008565, VSP 008567;
Note=Produced by alternative pplicing of isoform 2;
In Stage SPECIFICITY: Ubjectious: Expressed prior to callularization in stage 3 embryos, and in blastoderm cells, including pole cells. Expressed throughout the rest of embryogenesis. Later, it is expressed at higher level in epidermal cells and CNS.
DEVELOPMENTAL STAGE: Isoform 3 is expressed both maternally and
                                                                                                                                                                                                                                                      Development 130:3125-3135 (2003).

-I- FUNCTION: Probable corepressor protein, which regulates different key pathways such as the EGF receptor and wig pathways. Involved in neuronal cell fate, survival and axon guidance, cell cycle regulation and repression of head identity in the embryonic trunk. May act with the Hox gene Deformed and the EGF receptor signaling pathway. Positive regulator of the Wig pathway in larval tissues but not in embryonic tissues. May act as a transcriptional corepressor protein, which repress transcription via the recruitment of large complexes containing histone deacetylase
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--- SIMILARITY: Belongs to the Spen family.
--- SIMILARITY: Contains 3 RNA recognition motif (RRM) domains.
--- SIMILARITY: Contains 1 SPOC domain.
--- CAUTION: It is uncertain whether Met-1 or Met-7 is the initiator.
                                 EGF receptor pathway,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   produced by use
                                                                                                                            FUNCTION ON WG PATHWAY.
MEDLINE=22668876; PubMed=12783785;
Lin H.V., Doroquez D.B., Cho S., Chen F., Rebay I., Cadigan K.M., "Splits ends is a tissue/promoter specific regulator of Wingless
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           008566;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins.
SUBCELULAR LOCATION: Nuclear.
ALTENATIVE PRODUCTS:
Comment=2 isoforms, 1 (shown here) and 2, are 1 alternative promoters.
Event-Alternative splicing; Named isoforms=4;
Name=1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Note=No experimental confirmation available;
Chen F., Rebay I.;
"split ends, a new component of the Drosophila E regulates development of midline glial cells.";
Curr. Biol. 10:943-946(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IsoId=Q8SX83-2; Sequence=VSP_008565, VSP_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO; GO:0007411; P:axon guidance; IMP.
GO; GO:0008347; P:glia cell migration; IMP.
InterPro; IPR00504; RNA_rec_mot.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IsoId=Q8SX83-1; Sequence=Displayed;
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SMARY; SM00360; RRM; 3.
PROSITE; PS50102; RRM; 3.
PROSITE; PS00030; RRM_RNP_1; FALSE_NEG.
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EMBL; AE003590; AAF51534.2; -.
EMBL; AE003590; AAF51535.2; -.
EMBL; AE003590; AAN10511.1; -.
EMBL; AY094788; AAN1141.1; ALT_SEQ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF188205; AAF13218.1; -.
EMBL; AF184612; AAF26299.1; -.
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2216 KNSSSHISRPHGCGGSSASSSKHHRRDKHAQKGSASSIETNSSIEVVVDDISQTKHNIN 2275
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       59 AMASSGOIDLLERLKEINLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSF 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      260 QNEGQGVGEINMATSGNGQGSTTRMDHETASVLSSSSTHSAPRRLTSHLGTKVEM---VY 316
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          537
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 419 TCWEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQAIAEL 478
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 154 EKDWYYAQLQNLTKRIDSLPLTENFSLQTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               538 EDLOQVIASVLRNLSWRADVNSKKTLREVGSVXALMECALEVKKESTLKSVLSALWNLSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 AAASYDQLLKQVE---ALKMENSNIRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDE
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                                                                                                                                                                                                                                                                                                 Query Match
3.3%; Score 474; DB 1; Length 5560;
Best Local Similarity 18.5%; Pred. No. 8.3e-10;
Matches 621; Conservative 479; Mismatches 1219; Indels 1034;
Transcription regulation; Repressor; Developmental protein;
Nuclear protein; Repeat; RNA-binding; Coiled coil;
Alternative promoter usage; Alternative splicing.
DOMAIN 554 632 RNA-BINDING (RRM) 1.
DOMAIN 656 730 RNA-BINDING (RRM) 2.
DOMAIN 734 806 RNA-BINDING (RRM) 3.
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2630 VSSGATNGAESKTLIYQMAPAVSKTEDVWVRIEDC--PINNPRSGRSPT-GNTPPVIDSV 2686
                        2687 SEKANPNIKDSKDNQAKON------VGNGSVPMRTVGLENRLNSFIQVDAPD-QK 2734
                                                                                                                                                             2735 GTEIKP---GON------NPV------PVSETNESSIVERTPFSSSSSK 2769
                                                                                                                                                                                                     4541 GAQTPPRRSGRNAQAKKTDAVQIINAVGRPRRSKDRKTIGEQTANLİBEVTASNATVAAS 4600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=99246063; PubMed=10231032;
Nagase T., Ishikawa K.-I., Suyama M., Kikuno R., Hirosawa M.,
Nagase T., Ishikawa K.-I., Suyama M., O'nara O.;
Miyajima N., Tanaka A., Kotani H., Nomura N., O'nara O.;
"Prediction of the coding sequences of unidentified human genes. XIII.
The complete sequences of 100 new cDNA clones from brain which code for large proceins in vitro.";
DNA Res. 6:63-70(1999).
                                                                                                         4497 SESC--NTRKSRRLOBKEDRSTVDDIIEDVVRNTNTPTGT------GPHLPK
                                                                                                                                                                                                                                                                                                                                                                                      MINT HUMAN STANDARD; PRT; 3664 AA.
Q96758; Q9H9A8; Q9UQ01; Q9Y5S6;
10-OCT-2003 (Rel. 42, Created)
10-OCT-2003 (Rel. 42, Last sequence update)
10-OCT-2003 (Rel. 42, Last sequence update)
MSX2-interacting protein (SMART/HDACI associated repressor protein).
MINT OR SHARP OR KIAA0929.
HOMO sapiens (Human).
                                                                                                                                                                                                                                              2770 HSSPSGTVAAR-------VTPFNYNPSPRKSSADSTSARPSQIP 2806
                                                                                                                                                                                                                                                                             4601 HLAPPEGAGVESHVPQLDAKEVEPVSVVTPIS-TPAPVSVAAPVTVPVPAMVP 4652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A., FUNCTION, SUBCELLULAR LOCATION, INDUCTION, RNA-BINDING, AND INTERACTION WITH NCOR2; HDAC1; HDAC2; RBBP4; MBD3;
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TISSUE Embryo, and Teratocarcinoma;

TISSUE Embryo, and Teratocarcinoma;

TISSUE T., Ota T., Hayashi K., Sugiyama T., Otsuki T., Suzuki Y.,

Nishikawa T., Nagai K., Sugano S., Takahashi-Fujii A., Hara H.,

Tanase T., Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K.,

Arita M., Nabekura T., Ishii S., Kawai Y., Saito K., Yamamoto J.,

Akamantau A., Nakamura Y., Nagahari K., Masuho Y., Oshima A.;

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Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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IISSUE=Liver, and Pituitary;

MEDLINE=21211190; PubMed=11331609;

MEDLINE=21211190; N. Xie W., Xie W.-Y., Ordentlich P., Tsai C.-C.,
HON M., Evans R.M.;

Hon M., Evans R.M.;

"Sharp, an inducible cofactor that integrates nuclear receptor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 294-3664 FROM N.A.
Rhodes S., Huckle E.;
Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
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Submitted (JUN-2003) to the EMBL/GenBank/DDBJ databases.
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INTERACTION WITH PPARD.
MEDLINE=21874127; Pubmed=11867749;
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Genes Dev. 15:1140-1151(2001).
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Ph. Sh. Y. Hon M. Fears R. M.

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The Continue and the Continue of transcriptional repression and nulsar receptor signaling.

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645 DSRRDYPARGREFYSEWETYQCDYYESRYYDDPI 1138 DKPTNYSERYSEBEQHEBERPTHYSIKYNEEKG 700 RERERREFESDDRDHEBERPIERSQSPI 1135 FSFSKSSGOSSK	1181 QMEMEIAKSEKFGSPKKÜUDEYERRELÜHBE 1676RGGAGGEFEKRDITPTEGRST 1238 CTKRERNYRSSRQISEDSERTGGSPSVRH 1717 KABEGDILAECINSAMPKGKSHKDFRVKKIMDO 1294 VLPYSNITVRESSLKFNPYDSSRREGWADM 1772PTGSPVKPIPONTEYRTRVRKNADSKNULL 1351 FDVSFPNSIIKRDSIRKRSVRDL 1821
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645	DSRRDYPARGREFYSEWETYQGDYYES DKPTNYSERYSEBEQHEREERPTNYSI
700	: : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
1195	FSFSKSSSGOSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQ 1237 :
1238	SRSGQPQKAATCKVSSINQETIQTYCVEDTFICFSRCSSLSSLSSAEDBIGGNQTTQE 1295
1296 872	ADSANTLQIAEIKEKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSSLSS 1344 : : :
1345	-ESARHKAVEFSSGAKSPSKGGAQTPKSPEHYVQETPLMFSRCTSVSSLDSFESRS 1400
1401	IASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPPQTAQTKREVPKNKA 1457
1458	PTABKRESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEP 1514 :
1515	FIGKDVELRIMPPVQENDNGNETESEQPKESNENQEKBAEKTIDSEKDLLDDSDD 1569 :: : :
1570	DDIEILEE-CIISAMPTKSSRKAKKPAQTASKLPPEVARKBSQLPVYKLLFSQNRLQP 1626 : ::
1627	OKHUSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGV 1675
1676	RGGAQSGEFEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDN 1716
1717	KABEGDILABCINSAMFKGKSHKPFRVKKIMDQVQ-QASASSSAPNKNQLDGKKKK 1771 :
1772	PTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKDSKKQNLKNNS 1820
1821	KDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSL 1862
1863 1455	SSIDFDDDDVDLSREKAELRKAKENKESEAKVTS 1896
1897	HTELTSNQOSANKTQALAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDE 1949
1950	KLONFALENTPVCFSHNSSLSSLSDIDGENNNKENBPIKETBPDSGGEPSKPQASGYAP 2009
2010	KSPHVB-DTPVCFSRNSSLSSUSIDSEDDLLQECISSAMPKKKKPSBLKGDNEKHSPRNM 2068 ::

protein)

Mus musculus (Mouse). Mus musculus (Mouse). Bukaryota, Merazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus

NCBI_TaxID=10090;

Msx2-interacting protein (SMART/HDAC1 associated MINT OR SHARP OR KIAA0929,

FUNCTION, SUBCELLULAR AND INTERACTION WITH MSX2

NF 49-3644 FROM N.A. (ISOFORM 1), TISSUE SPECIFICITY, DNA-BINDING,

TISSUE=Testis;

SEQUENCE OF COCATION, MEDLINE=99379811; PubMed=10451362;
Newberry E.P., Latifi T., Towler D.A.;
"The RRM domain of MINT, a novel msx2 binding protein, recognizes regulates the rat osteocalcin promoter.";
Biochemistry 38:10678-10690(1999).

SEQUENCE OF 1-112 FROM N.A.

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                GGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQA 2128
                                                                                                                                                                                                        ---PDŠTQPLŠK 1761
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                                                                                                                2030 PKAABEBEAGSEQKRDRKDAGTDKNPPETAP-VEVVEKKPAPEKNSKSKRGRSRN-SRLAV
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                                                                                                                                                                  2189 KGGKKVYKSLITGKVRSNSEISGQMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSK
                                                                                                                                                                                                                                            2249 KGPPLKTPASKSPSEGOTATTSPRGAKPSVKSELSPVARQTSO-------
                                                                                                                                                                                                                                                                            -----PAQKSEEANE-----PKAEKPDATADAEPDANQKAEAAPESQPPASEDLEVDP
                                                                                                                                                                                                                                                                                                                    -IGGSSKAPSRSGSRDSTPSRPA----QQPLSRPIQSPGRNSISPGRNGISPPNXLSQL
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Adachi J., Alzawa K., Akimura T., Arakawa T., Carninci P., Fukuda S., Hashizume W., Hayashida K., Hirozane T., Hori F., Imotani K., Ishii Y., Itoh M., Kagawa I., Kawai J., Kojima Y., Kondo S., Konno H., Koya S., Miyazaki A., Murata M., Nakamura M., Nomura K., Numazaki R., Ohno M., Ohsato N., Saito R., Sakazume N., Sano H., Sasaki D., Sato K., Shibata K., Shiraki T., Tagami M., Takeda Y., Waki K., Watahiki A., Muramatsu M., Hayashizaki Y.,

Σ

Sakamoto T., Gotou T., Isagawa Y., Mimura H., Kimura K., Kawaichi "MINT/spen negatively regulates Notch signaling by inhibiting RBP-J/Su(H) activity.";

Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.

SEQUENCE OF 69-3644 FROM N.A. (ISOFORM 2), AND VARIANTS THR-348, PHE-762; PHE-773 AND LEU-933. STRAIN=ICR; TISSUE=Brain;

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Dillinger K.,
W., Liptay S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUNCTION, AND TISSUE SPECIFICITY.

MEDLINE=22483652; PubMed=1254956;

Kuroda K., Han H., Tani S., Tanigaki K., Tun T., Furukawa T.,

Taniguchi Y., Kurooka H., Hamada Y., Toyokuni S., Honjo T.;

"Regulation of marginal zone B cell development by MINT, a suppressor of Nocch/RBP-J signaling pathway.";

Immunity 18:301-312(2003).

-i- FUNCTION: Essential corepressor protein, which probably regulates different key pathways such as the Notch pathway. Negative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene:
                                                                                                                     Vago
                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=22579291; PubMed=12693553; MEDLINE=22579291; PubMed=12693553; Medajima N., Kikuno R., Ohara R., Inamoto S., Aizawa H., Yuasa S., Nakajima D., Nagase T., Ohara O., Koga H.; Koga H.; Macini Le coding sequences of mouse homologues of KIAA ger II. The complete nucleotide sequences of 400 mouse KIAA-homologous randomly sampled from size-fractionated libraries of cDNA clones randomly sampled from size-fractionated libraries.";
                                                                                                             Ripoll C., Vaç
Mattei M.-G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE SPECIFICITY.
MEDLINE-22261914; PubMed=12374742;
Oswald F., Kostezka U., Astrahantseff K., Bourteele S., Dilling Zechner U., Ludwig L., Wilda M., Hameister H., Knoechel W., Lik Schmid R.M.;
"Schmid R.M.;
"StharP is a novel component of the Notch/RBP-Jkappa signalling
                                                                MEDLINE 97237053; PubMed=9119401;
Crozet F., Bl-Amraoui A., Blanchard S., Lenoir M., Ripoll C., Wardel C., Fizames C., Levi-Acobas F., Depetris D., Mattei M., Weil D., Pujol R., Petit C.;
"Cloning of the genes encoding two murine and human cochlear unconventional type I myosins.";
                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 2598-3644 FROM N.A.
SEQUENCE OF 318-578 FROM N.A.
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                                        rissum=Cochlea;
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MINT_MOUSE STANDARD; PRT; 3644 AA. Q62504; Q80TN9; Q99PS4; Q9QZW2; 10-0CT-2003 (Rel. 42, Created) 10-0CT-2003 (Rel. 42, Last sequence update) 15-WAR-2004 (Rel. 43, Last annotation update)

MINT_MOUSE ID MINT_MC AC Q62504, DT 10-OCT-DT 10-OCT-DT 15-MAR-

RESULT 7

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regulator of the Notch pathway via its interaction with RBPSUH, which prevents the association between NOTCH1 and RBPSUH, and therefore suppresses the transactivation activity of Notch signaling. Blocks the differentiation of precursor B cells into marginal zone B cells. Probably represses transcription via the recruitment of large complexes containing histone deacetylase proteins. May bind both to DNA and RNA.

-!- SUBUNIT: Interacts with the nuclear receptors RAR and PPARD interacts with RAR in absence of ligand. Bind to the steroid receptor RNA coactivator SNA (By similarity). Interacts with MSX2. Interacts with RBPSUH; this interaction may prevent the interacts with RBPSUH and NOTCH1.

-!- SUBCELLULAR LOCATION: Nuclear. Associates with chromatin.

-!- ALTERNATIVE PRODUCTS:

Event-Alternative splicing; Named isoforms-2;
                                                                                                                                                                                                                                                                                                                                                                                                        Isode 262504-2; Sequence - VSP 008564;
Isode 262504-2; Sequence - VSP 008564;
Note = No experimental confirmation available;
Note = No experimental confirmation available;
TISSUE SPECIFICITY: Highly expressed in testis. Expressed at lower level in brain, lung, spleen, liver and kidney. Weakly expressed in cardiac and skeletal muscles and ovary. In spleen, it is spressed in follicular B-cells, while it is weakly expressed in marginal zone B-cells.
DOMAIN: The RID domain mediates the interaction with nuclear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -. DOMAIN: The SPOC domain, which mediates the interaction with NCOR2, is essential for the repressive activity (By similarity).
-!- SIMILARITY: Belongs to the Spen family.
-!- SIMILARITY: Contains 1 RID (receptor interacting) domain.
-!- SIMILARITY: Contains 1 RPOC domain.
-!- SIMILARITY: Contains 1 SPOC domain.
-!- SIMILARITY: Contains 1 SPOC domain.
-!- CAUTION: Ref.4 sequence differs from that shown due to multiple frameshifts and conflicts that create stop codons.
-!- CAUTION: Ref.5 sequence differs from that shown due to what seems to be the presence of intronic sequence in the cDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGD; MGI:1891706; Mint.
InterPro; IPR00504; RNA_rec_mot.
Pfam; PF00076; rrn; 3.
PRAST: SN00360; RRM; 3.
PROSITE; PS50102; RRM; 4.
PROSITE; PS50102; RRM RNP_1; FALSE_NEG.
PROSITE; PS50917; SP06; 1.
PROSITE; PS50917; SP06; 1.
PRASTE; PS50917; SP06; 1.
RNA-binding; Repeat; Coiled coil; Alternative splicing; Polymorphism.
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Name=2;
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EMBL, ARF156529, AAD55931.1; ALT_INIT.
EMBL, AB055980; BAB32786.1; ALT_EMBL;
EMBL, Z78160; CA801562.1; ALT_SEQ.
EMBL, AK122402, BAG55684.2; ALT_SEQ.
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982 S----IESYSEDDESK----FCSYGQY------PADLAHKIHSAN 1012
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
2.9%; Score 428.5; DB 1; Length 3644;
Best Local Similarity 18.7%; Pred. No. 2.4e-08;
Matches 522; Conservative 325; Mismatches 903; Indels 1047; Gaps 126;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       727 RNLMANRPAK-YKDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLSPK--A 783
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         844 SRSEKDRSLERERGIGLGNYHPATENPGTSSKRGLQISTTAAQIAKVMEE----
                                                                                                                                                             WITH MSX2.
WITH RBPSUH
                                                                                                                                      Missing (in isoform 2) /FTId=VSP_008564.
 INTERACTION
                             ARG-RICH.
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		2158 PTSNKGPRILK 2060 PSTDKGGPDTFPVEVLERK 2206 NSEISGGMKOPLQANMPSI 2119 DKEAGPAASPQESESPOK 2246VSKKGPPL 2175 RQIELEQAVQNIAKLBEPS 2292IGGSSKAPSRSG 2291 AAAIGSIISDASGEFENFS	2331 PGRNGISPPNKLSQLPRTS 2289 PQVSALDPPGGSADTKETR 2391 IPRSESASKGLNQMNNGNG 2340RKRN 2451 TLRRKLEESASFESLSPS 2451 TLRRKLEESASFESLSPS 2382EEKPSE 2382EE	
8 8 8 8 8 8 8	4 8 8 8 8 8	8 8 8 8 8 8 8	8 6 6 6 6	3 8 5 8 5 8 5
1053 KHILEDEIKQS-EQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQGECVSPYRSR 1105 637 PHKCREERRGSYEYSGETTYXENVTTPTTYPVYTESTDDKHLKFQPHFGQGECVSPYRSR 1105 636 PHKCREERRGSYEYSGETTYXENVTTPTTYPVYTESTDDKHLVSERYSEE 1150 678 G		1387		1715DNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSAPNKN 1763
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                                              2720 NRLNSPIQUDAPDQK-GTEIKPG----QNNPVPVSETNESSIVERTPPSSSSSKHSSP 2773
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                                                                                 TISSUE=Lens epithelium;

MEDIINE=90520161; PubMed=1694016;

MEDIINE=90520161; PubMed=1694016;

Makamura T., Donovan D.M., Hannada K., Sax C.M., Norman B.,

Flanagan J.R., Ozato K., Westphal H., Piatigorsky J.;

"Regaliation of the mouse alpha A-crystallin gene: isolation of a cDNA encoding a protein that binds to a cis sequence motif shared with the major histocompatibility complex class I gene and other genes.";

Mol. Cell. Biol. 10:3700-3708[1990].

PALINDROMIC SEQUENCE 5'-GGGAAATCCC-3' IN THE ALPHA-A CRYSTALLIN
                                                                                                                                                                                                                                                                                                                                                                              01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Zinc finger protein 40 (Transcription factor alphaA-CRYBPI) (Alpha A-CRYSPI) (Alpha A-HVSPI OR ZNF40 OR CRYABPI).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SUBCELLULAR LOCATION: Nuclear.
DOMAIN: CONTAINS TWO SETS OF 2 ZINC-FINGERS, WHICH ARE WIDELY
SEPARATED AND RECOGNIZE THE SAME DNA SEQUENCE. THERE IS A FIFTH
ZINC-FINGER IN-BETWEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Brady J.P., Kantorow M., Sax C.M., Donovan D.M., Piatigorsky J.; "Murine transcription factor alpha A-crystallin binding protein I. Complete sequence, gene structure, expression, and functional inhibition via antisense RNA."; J. Biol. Chem. 270:1221-1229 (1995).
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
----PPLEGVSAAAVPN----ADTQASE-
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EMBL; L36825; AAA98810.1; JOINED.
EMBL; L36826; AAA98810.1; JOINED.
EMBL; L36827; AAA98810.1; JOINED.
EMBL; L36828; AAA98810.1; JOINED.
EMBL; X68946; CAA48762.1; -.
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MGD; MGI:96100; Hivepl. InterPro; IPR007087; Znf C2H2. Pfam; PF00096; zf-C2H2; 5.

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R PROSITE; PRODGS; ZnF_C2H2; 5.

R PROSITE; PS50159; ZINC_FINGER_C2H2_1; 4.

R PROSITE; PS50157; ZINC_FINGER_C2H2_2; 4.

W Transcription regulation; ZINC_FINGER_C2H2_2; 4.

W Nuclear protein; Repeat.

ZN FING 407 429 C2H2_TYPE.

T ZN FING 407 429 C2H2_TYPE.

T ZN FING 435 459 C2H2_TYPE.

T ZN FING 435 976 C2H2_TYPE.

T ZN FING 953 976 C2H2_TYPE.

T ZN FING 2074 2096 C2H2_TYPE.

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8.4%; Pred. No. 1.3e~07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                        Pukuyama R., Rapoport S.I.;
"Brain-specific expression of human microtubule-associated protein 1A
"Brain-specific expression of human chromosome 15.";

(MAPLA) gene and its assignment to human chromosome 15.";

J. Neurosci. Res. 40.820-825(1995).

-!- FUNCTION: Structural protein involved in the filamentous cross-bridging between microtubules and other skeletal elements.

-!- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate with MAPLA and MAPLA proteins.

-!- TISSUE SPECIFICITY: Brain.
                                                                                                                                                                                                                                                                                                                       DOMAIN: The basic region containing the repeats may be responsible for the bhinding of MAPIA to microtubules.

FITH: Various serine residues may be phosphorylated by CAMP kinase. PTM: LC2 IS COEXPRESSED WITH MAPIA. IT IS A POLYPEPTIDE GENERATED FORM MAPIA BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH SIMILARITY: TO MAPIB.
                         Ohtani K., Rutherford T., Sakamoto H., Naftolin F.; "Microtubule associated protein 1A (MAPIA) in human brain sequence and physiological role."; Submitted (NOV-1996) to the BMBL/denBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LYS-RICH (BASIC).
9 X 3 AA REPEATS OF K-K-[DE]
                                                                                       SEQUENCE OF 134-419 FROM N.A.
IISSUB=Fetal muscle;
Chiannilkulchai N., Pasturaud P., Richard I., Auffray C.
                                                                                                                                Beckmann J.S.;
Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MIM; 600178; -.
GO; 60:005875; C:microtubule associated complex; TAS.
Morrotubule; Repeat; Phosphorylation.
CHAIN :2490 2805 MAPL_LIGHT_CHAIN LC2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VV -> IP (IN REF. 4).

A -> G (IN REF. 4).

V -> A (IN REF. 4).

O -> H (IN REF. 3).

S -> G (IN REF. 3).

K -> G (IN REF. 4).

AK -> ST (IN REF. 1).

AK -> ST (IN REF. 1).
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Phosphorylation.

MAP1 LIGHT CHAIN LC2
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V - V
                                                                                                                                                                                             MEDLINE=95356255; PubMed=7629894;
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                                                                                                                                                                      1607-1883 FROM N.A.
SEQUENCE OF 78-1687 FROM N.A.
TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; U38291; AAB41132.1; -.
EMBL; U38292; AAB41133.1; -.
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               ENCAND - ANAMAN (IN REF. 1).

E - D (IN REF. 3).

E - D (IN REF. 3).

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E - D (IN REF. 3).

TK -> SG (IN REF. 3).

TK -> SG (IN REF. 3).

TK -> R (IN REF. 3).

TK -> R (IN REF. 3).

TK -> R (IN REF. 3).

TK -> R (IN REF. 3).

TK -> R (IN REF. 1).

Q -> K (IN REF. 1).

Q -> K (IN REF. 1).

TYLPGAITSPD -> EVLIWGDHQALN (IN REF. 3).

MISSING (IN REF. 1).

A -> T (IN REF. 3).

A -> T (IN REF. 1).

G -> V (IN REF. 1).

G -> V (IN REF. 1).

G -> V (IN REF. 1).

G -> V (IN REF. 1).

G -> V (IN REF. 1).

G -> V (IN REF. 5).

G -> W, FIREN -> AHSRV (IN REF. 5).

G -> W, FIREN -> AHSRV (IN REF. 5).
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2.8%; Score 401.5; DB 1;
Best Local Similarity 18.2%; Pred. No. 1.7e-07;
Matches 523; Conservative 382; Mismatches 1149;
-> KKKRINS
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10.08 STITO

1890	SEAKVISHTELISNQQSANKIQAIAKQPINRGQPKPILQKQSTFPQSSKDIPDRGAATDE 1949 SEKLIRSPFEIISPPASPPEMVGQRVPSAPGQESPIPDP 1823
1950	KLONFAIENTFVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPDSQGEPSKFQASGYAP 2009
2010	KSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKPSRLKGDNEKHS 2064 :
1920	PRIMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFDWKAIQEGAN 2109
2110	SIVSSLHQAAAAACLSRQASSDSDSILSLKSGISLGSPFHLTPDQEEKPFTSNKGP 2165QMMLTGLGPACPTREPPLGAAGDWPPCLSTKEAAAGRNTSAEKELSSPISP 2023
2166	RILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMKOPLQANMPSIS 2225
2226	RGRIMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSPSBGGTATTSPRGAKPSVK 2279
2280	SELSPVARQTSQIGGSSKAPGRSGSRDSTPSRPAQQPLSRP1QS 2323
2324	PGRNSISPGRNGISPPSPG 2370
2371	RQMSQQNLTKQTGLSKNASSIPRSES-ASKGLNQMNNGANKKVELSRMSSTKS 2424
2425 2256	SGSESDRSERPVLVRQSTFIKEAPSPTLRRKLEESAAFESLSPSSR 2470
2471	PASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG 2520
2521	RPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSLERVSTWRRTGSSSSILSA 2576
2577	SSESSEKAKSEDEKHVNSISGT
2618	NEFSPINSTSQIVSSGATNGAESKTLIYOMAPAVSKTEDVWYRIEDCP 2665 TTGXPXPVIDETPPTSASDSGSSOSDSDVPPETEECPSITAEAALDSDE 2535
2666	INNPRSGRSPTGNTPPVIDSVSEKANPNIKDSKDNQAKQNVGNGS 2710
2711	VPMRTVGLENRLNSFLQVDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPFSSSSSKH 2770
2771	SSPSGTVAARVTPFNYNDSPRKSSADSTSARPSQIPTPVNNNTKKRDSKTDSTESSG 2827

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HSSP; P42771; IDC2.
Genew; HGNC:493; ANK2.
MIM; 106410; -.
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Matches 426; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Name=3;
Isoid=Q01484-3; Sequence=VSP 000268;
Isoid=Q01484-3; Sequence=VSP 000268;
-: TISSUE SPECIFICITY: Plasma membrane of neurons as well as glial cells throughout the brain.
-: PTM: Phosphorylated at multiple sites by different protein kinases and each phosphorylation event regulates the protein's structure and function (Potential):
-: SIMILARITY: Contains 13 ANK repeats.
-: SIMILARITY: Contains 1 death domain.
                                                                                                                                                                                                                                                                                                                                 TISSUE=Brain stem,
MEDLINE=94075409; PubMed=8253844;
Chan W., Kordell E., Bennett V.;
"440-kD ankyrinB: structure of the major developmentally regulated domain and selective localization in unmyelinated axons.";
J. Cell Biol. 123:1463-1473(1993).
                                                                                                                              Eukaryoča, Metazoa: Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE OF 463-495 FROM N.A.
MEDLINE=92009921; PubMed=1833308;
Tse W.T., Menninger J.C., Yang-Feng T.L., Francke U., Sahr K.E.,
Lux S.E., Ward D.C., Forget B.G.;
"Isolation and chromosomal localization of a novel nonerythroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ankyrin gene.";
Genomics 10:858-866(1991).
-!- FUNCTION: Attach integral membrane proteins to cytoskeletal
-!- Alto bind to cytoskeletal proteins.
-!- ALTERNATIVE PRODUCTS:
Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                  MEDLINE=91302466; PubMed=1830053;
Otto E., Kunimoto M., McLaughlin T., Bennett V.;
"Isolation and characterization of cDNAs encoding human brain
ankyrins reveal a family of alternatively spliced genes.";
J. Cell Biol. 114:241-253(1991).
                                  Old Has, SIANDARD; PRT; 3924 AA.

Q01484; QOLH85;

Q01-APR-1993 (Rel. 25, Created)

O1-OCT-1996 (Rel. 34, Last sequence update)

28-FEB-2003 (Rel. 41, Last annotation update)

Ankyrin 2 (Brain ankyrin) (Ankyrin B) (Ankyrin, nonerythroid)
                                                                                                                                                                                                                                                                                      Carpenter S.;
Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q01484-2; Sequence=VSP_000267, VSP_000268;
                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS 1, 2 AND 3).
TISSUE=Brain stem;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=Q01484-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X56957; CAA40278.1; -. EMBL; X56958; CAA40279.2; -. EMBL; Z26634; CAA42644.1; -. EMBL; M37123; AAA62828.1; -. PIR; S37431; S37431.
                                                                                                                   Homo sapiens (Human)
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                        ANK2 HUMAN
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Q -> QFLGKLHLPTAPPPLNEGESLVSRILQLGPPGTK
(in isoform 2).
/FTId=VSP 000267.
/FTId=VSP 000267.
/FTId=VSP 000268.
GQ -> PE (IN REF. 4).
I -> S (IN REF. 1).
QY -> HA (IN REF. 1).
I -> Y (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2.7%; Score 399; DB 1; Length 3924;
llarity 19.5%; Pred. No. 3.1e-07;
Conservative 311; Mismatches 803; Indels 644; Gaps
52AC496C428E29D2 CRC64;
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SEQUENCE FROM N.A. (ISOFORMS, VO AND V1).

STRAIN=White legions; TISSUB-Limb bud;

MEDLINE-93300846; PubMed-8314802;

A Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura T., Nishida Y., Ito K., Kimata K.;

Shinomura T., Nishida Y., Ito K.,

The expressed during chondropenesis in chick limb buds. Alternative spliced multiforms of PG-M and their relationships to versican. ";

Then, Cabe., 268-1446-14469(1993).

The regulation of Cell motility, growth and differentiation. Binds the regulation of cell motility, growth and differentiation. Binds hyaluronic acid.

-! SUBCELLULAR LOCATION: Secreted, extracellular matrix.

-! ALTERNATIVE PRODUCTS:

Comment-Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                     Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                developing limb buds.
DEVELOPMENTAL STAGE: Disappears after the cartilage development
                                                      PGCV CHICK STANDARD, PRT; 3562 AA.
090953; 090945;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last sequence update)
10-OCT-2003 (Rel. 42, Last annotation update)
Versican core protein precursor (Large fibroblast proteoglycan)
(Chondroithn sulfate proteoglycan core protein 2) (PG-M).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -:- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
-:- SIMILARITY: Contains 2 link domains.
-:- SIMILARITY: Contains 2 ESP-like domains.
-:- SIMILARITY: Contains 1 C-type lectin family domain.
-:- SIMILARITY: Contains 1 Sushi (SCR) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=090953-2; Sequence=VSP 003093;
TISSUE SPECIFICITY: Prechondrogenic condensation area of
                                                                                                                                                                                                                                                                                                                                                                                                                                    IsoId=Q90953-1; Sequence=Displayed;
3195 VQTGDIPPLSG--VKQISCPDSSE 3216
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EMBL, D13542; BAA02742.1; --
ERRI, D13542; BAA02742.1; --
HSSP, P00740; LEDM.
INTERPRO, IPR000152; Asx hydroxyl_S.
INTERPRO, IPR000742; EGF_2.
INTERPRO, IPR000742; EGF_1ke.
INTERPRO, IPR0001881; EGF_1ke.
INTERPRO, IPR007100; IGP_1ke.
INTERPRO, IPR007100; IGP_1ke.
INTERPRO, IPR007100; IGP_1ke.
INTERPRO, IPR001399; Link.
INTERPRO, IPR001399; Link.
INTERPRO, IPR000436; Sushi_SCR_CCP.
Pfam; PF00008; EGF; 2.
Pfam; PF00008; EGF; 1.
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                                   RESULT 11
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EGF-LIKE 1.
EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL)
                                                                                                                                                                                                                                           Glycoprotein; Proteoglycan, Lectin; Extracellular matrix; Sushi; Signal; Repeat; EGF-like domain; Calcium; Immunoglobulin domain; Hyaluronic acid; Alternative splicing.
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485 1411 Missing (in isoform V1).
FTTd=VSP 00303.
3562 AA; 388078 MW; 9BC566E88C1602D2 CRC64;
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IG-LIKE V-TYPE.
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Pfam; PF00084; sushi; 1.
Pfam; PF00193; Xlink; 2.
PRINKT; PR01265; LINKMODULE.
ProDom; PR000318; Link; 2.
SWART; SW00032; CCP; 1.
SWART; SW00034; CLECT; 1.
SWART; SW00409; IG; 1.
SWART; SW00409; IG; 1.
SWART; SW00446; LINK; 2.
PROSITE; PS00010; CTYPE_LECTIN, 1.
PROSITE; PS00010; CTYPE_LECTIN, 1.
PROSITE; PS00026; EGF 2; 1.
PROSITE; PS00026; EGF 2; 1.
PROSITE; PS00026; EGF 2; 1.
PROSITE; PS00026; EGF 3; 2.
PROSITE; PS0026; EGF 3; 2.
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PROSITE; PS0026; EGF 3; 2.
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ò	1270	CFSRCSSLSSAEDEIGCNQTTQEADSANTLQIAEIKEKIGTRSAEDPVSEVPAVSQH 1329
QQ	1568	AMLEPVYSGESEVTTTDKYLEITSVYEQSPKKNKETVMWH 1607
ò	1330	PRIKSSRLQGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPPEHYVQETPLMFSR 1386
ОР	1608	GTBESSTKDTKNLLLITNESSGDGSTESDLSRSVFTEILTMSSHEDSEKISH 1659
ò	1387 (CISVSSLDSFESRSIASSVQSEPCSGWVSGIISPSDLPDSPGOTMPPSRSKTPPPPPPQTA 1446
Ор	1660	TISVPILSVERSAVTAAPSADSDTATVGIDVKDLIPKGGTATPGNYYKSTI 1711
ò	1447 (QTKREVPKNKAPTAEKRESGPKQAAVN
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ò	1481	VLP-DADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPP 1527
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ò	1792	S-KNNLNAERVFSDNKDSKKQNLKNNSKDFNDKLPRNEDRV
QQ	2082	SPESUVNNSTLDTMVTHGTIRAVAESTESKKGKGSFSAVS 2121
ò	1843	PHHYTPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTEL 1900
οp	2122	LGKILMIEHGSGEELKVDSSTTKLMSNGPTEKLLGSHFSFFD 2163
δλ	1901	TSNQQSANKTQAIAKQPIN-RGQPKPILQKQSTFPQSSKDI 1940

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ALTERNATIVE PRODUCTS
                                                                                                                                                                      STANDARD;
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                                                                                                                                                                                                                                                                                                           Rattus norvegicus (Rat)
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1941 PDRGATDEKLONFAI-ENTPVCFSHNSSLSSLSDIDOENNNKENEPIKETEPP--DSQG
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-----NPYSNEQSTISSELLNTIELVTS 3223
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-!- SUBCELLULAR LOCATION: Concentrated at presynaptic side of synaptic
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Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORM 2), AND INTERACTION WITH RABACI.
MEDLINE-20170257; PubMed-10707984;
Fenter S.D., Chung W.J., Zhai R., Cases-Langhoff C., Voss B.,
Garner A.M., Kaempf U., Kindler S., Gundelfinger E.D., Garner C.C.,
"Piccolo, a presynaptic zinc finger protein structurally related to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  [3]
CALICUM-BINDING ACTIVITY, AND MUTAGENESIS OF ASP-4668; ASP-4674;
VAL-4688; MET-4689; VAL-4690; SER-4691; GLN-4692; ASN-4693 AND
ALA-4694.
MEDLINE=21181819; PubMed=11285225;
Gerber S. H., Garcia J., Rizo J., Suedhof T.C.;
"An unusual C(2)-domain in the active-zone protein piccolo:
implications for ca(2+) regulation of neurotransmitter release.";
EMBO J. 20:1605-1619(2001).
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-!- SUBUNIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IsoId=09JKS6-2; Sequence=VSP 003930, VSP 003931; DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change. SIMILARITY: Contains 2 C2 domains. SIMILARITY: Contains 1 PDZ/DHR domain.
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                                                                                                                                                                                                                                                                                                                                                                                                           0907656; Q9ULT1; Created) 28-FEB-2003 (Rel. 41, Created) 28-FEB-2003 (Rel. 41, Last sequence update) 42, Last annotation update) Piccolo protein (Multidomain presynaptic cytomatrix protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM 1).
Fenster S.D., Cases-Langhoff C., Gundelfinger E.D., Garn.
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
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Name=1;
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EMBL, AF27534; AAF63196.1; -.
HGS, P04410, 1A25.
GG, GO:00164202; C:synaptic junction; IDA.
GO; GO:0005509; F:calcium ion binding; IDA.
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                                                                                        2802 PSQIPTPVNNNTKKRDSKTDSTESSGTQSP
                                                                                                                                                                    SPSLPEVTNGSDFLIGTSVGSVEGTAVOIP
        3175 LGPLLGQQEITTISSNIATNNTAPGN--
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330 LAQTPGHGKFPLGPVKSPAQQPGTAKHPAQQPGPQTAAKVPGP 372 330 LAQTPGHGKFPLGPVKSPAQQPGTAKHPAQQPGPQ	1573 EILEECIISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRL 1624 1573 EILEECIISAMPTKSSRKAKKPAQTASKLP	1625 QPQKHVSFTPGDDMPRVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQS 1681	1682GEPEKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDI 1723	525 LCNTTELLLHIPEKANFNTCTECQSTVCSLCGFNPNPHLTEIKEMLCLNCQMQRALGGDL 584	1724 LAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDGKK	585	1770KKPTSPVKP	1779IPQNTEYRTRVRKNADSKNNLNAERVFSDNKDSKKKQNLKONSKDFNDKLPNNEDRV	105	1835 RGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDDVDLSREKAELRKAKEN 1887 : : :	1888 KESEAKVTSHTELTSNQQSANKTQAIAKQPINRGQPKPILQKQSTFPQS		1937 SKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKETEPPD	870 QPTTPQETVTGKLFGFGASIFSQASNLISTAGQQGFHPQTGPAAFSKQAPTP	1995 SQGEFSK-VQAGGTARKSFHVEDITYVCKSRNSSEDSELSEDSEDDLQEGISSAMRKKK 2052 922 SQSPAAQGPAKSTGQLPPAPAKATAVKKBAKAAAAENLESKPEQAPTAKKTEKDKK 977	2053 PSRLKGDNEKHSPRNMGGILGEDLTLDLKDIORPDSEHGLSPDSENFDWKA	978 PPPAKVGKPPPSEPEKAVPAHKPDKTTKPKPACPLCRTELNLG-SQEPPNFNT	2104 IQEGANSIVSSLHQAAAAACLSRQASSBDSDSILSLKSGISLGSPF 2148 1030 CTECKNQVCNLCGFNPTPHLTEIQEWLCLNCQTQRAISGQLGDMGKMPPAPSG-PKASPM 1088	2149HLTPDOEEKPFTSNKGPRILKPGEKSTLETKKIESES 2185	2186 KGIKGGKKYYKSLITGKYRSNSEISGQMKQPLQANMPSISRGRTMIHIP 2234	2235 GVRNSSSSTSPVSKKGPPLKTPASKSPSEGQTATTSPRGAKPSVKSELSPVARQTSQ1GG 2294	2295 SSKAPSRGGRDSTPSRPAQP : ::: :	2355 STKSSGSGKMSYTSPGRQMSQQNLTKQTGLSKNASSIPRS 2394
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OR GO: GO:0005544; F:calcium-dependent phospholipid binding; IDA. RGO: GO:0005522; F:profilin binding; ISS. RGO: GO:0007010; P:cytoskeleton organization and biogenesis; ISS. RGO: GO:0016080; P:synaptic vesicle targeting; NAS. R InterPro: IPR00048; C2. R InterPro: IPR00048; P: ST PR004889; Znf Piccolo	Pfam; PF001 Pfam; PF005 Pfam; PF057 SMART; SM00	SMART; SMOOZ PROSITE; PSOO PROSITE; PSSOO	Calcium/ph	DOMAIN 372 491	ZN_FING 523 547 C4-TYPE (PC ZN FING 1010 1033 C4-TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE (PC PC N TYPE PC PC N TYPE (PC PC N TYPE PC PC N TYPE PC PC N TYPE (PC PC N TYPE PC PC N TYPE PC PC N TYPE PC PC N TYPE PC PC N TYPE PC PC N TYPE PC PC N TYPE PC PC PC N TYPE PC PC PC PC PC PC PC PC PC PC PC PC PC	DOMAIN 4442 4536	DOMAIN VARSPLIC	VARSPLIC 4881 5085	T MUTAGEN 4668 4668 D->A, COMPLETE JOSS OF CALCIUM-BINDING ADD CALCTING-DEPRINENT PHOSPHOLIETE	T MUTAGEN 4674 4674 D->A: COMPLETE LOSS OF CALCIUM-BINDING AND CALCIUM-DEPENDENT PHOSPHOLIFID	MUTAGEN 4688 4688 VS::SMALL INCREASE I	MUTAGEN 4688 4689	MUTAGEN 4689 4689 MUTAGEN 4690 4691	MUTAGEN 4692 4693	MUTAGEN 4694 4694 SECITENCE 5085 AD. 552702 M	10, 12, 13, 10, 10, 10, 10, 10, 10, 10, 10, 10, 10	ocai Similarity 20.0%; Fred. No. is 386; Conservative 241; Mismat	/ 1187 IPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPSSNAKRQNQLHPSSAQSRSGQPQ 1244	7 1245 KAATCKVSSINQETIQTYCVEDTPICFSRCSSLSSLSSABDEIGCNQTTQEADS 1298 127 STISIKESKRRTDFKERYKSSMMPCFFSDNNPLANVSKVNNKRNPFN1.5GGFAGGF-FT 185	ANTLOIABIKEKIGTRSABDPVSEVPAVSQHPRTKSSRLQGSSLSSESARHKAV """" """ """ """ """ """ """ """ """	EFSGAKSPSKGGAQTPKSPPEHYVQETPLMFSRCTSVSSLDS	WVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQ	1470 AAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELR 1523

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                                                                                                                                                                               1481 GSSSSDEYKQEDSQGSGEBEDFIRKQIIEMSAD-EDASGSEDEEFIRSQLKEISGVGESQ 1539
                                                                                                                                                                                                      ENQVSAKGTWRKI--KENEFSPTNSTSQTVSSG--------ATNGA 2638
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                     2395 E-SASKGINOMNNGNGANKKVELSRMSSTKSSGSESDRSERPVLVRQSTFIKEAPSPTL- 2452
                                                                                                               PTIEYNDGRPAKRHDIARSHSESP---SRLPINRSGTWKREHSKHSSSLPRVSTWRRT-- 2567
1273 GSSKDGQGERSKEKTEKEEDKSDISSSQQPKSPQGLSDTGYSSDGISGSLGEIPSLIPSD 1332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-99-197764; PubMed-10508862; Wang X., Kibschull M., Laue M.M., Lichte B., Petrasch-Parwez E., Kilimann M.W.; M. Laue M.M., Lichte B., Petrasch-Parwez E., Kilimann M.W.; M. Aczonin, a S50-kd putative scaffolding protein of presynaptic active zones, shares homology regions with rim and bassoon and binds profilin.";
                                                                                                                                                                                                                                                                                                             2453 RRKLEESASFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLS
                                                                               GSSSS-----ILSASSESSEXAKSEDEKHVNS---ISGTKQSK
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                                                                                                                                                                                                                                                   ESKTLIYQMAPAVSKTEDVWVRIEDCPINNPRSGRSPTGNTPPVIDSVSEKANPNIKDSK
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                                          1333 EKDLLKGL-----SILEAQASTLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prediction of the coding sequences of unidentified human genes. IX.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nagase T., Ishikawa K.-I., Miyajima N., Tanaka A., Kotani H.,
Nomura N., Ohara O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE OF 552-4404 FROM N.A.
Kraemer J., Wollam C., Wohldmann P., McGrane B.;
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STANDARD, PRT, 5147 AA. 2976V0; 043373; 060305; 09BVC8; 09UV2; 09Y6U9; 28-FEB-2003 (Rel. 41, Created) 10-0CT-2003 (Rel. 41, Last sequence update) 10-0CT-2003 (Rel. 42, Last annotation update) Piccolo protein (Aczonin) (Fragments). PCLO OR ACZ OR KIAA0559.
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                                                                                                                                                                                                                                                                                                                       1656 EDRSR---GEGSSSLH----
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                                                                                                                                                                                                   MEDINE-238825; PubMed-12477932;

MEDINE-238825; PubMed-12477932;

Altachul S.P., Feingold E.Z., Wagner L., Shenmen C.M., Schuler G.D.,

Altachul S.P., Zeeberg B. Buetow K.H., Schaefer C.R., Bhat N.K.,

Altachul S.P., Zeeberg B. Buetow K.H., Schaefer C.R., Haich B. M.

Altachul S.P., Zeeberg B. Buetow K.H., Schaefer C.R., Haich B. M.

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.

Stapleton M., Soares M.B., Bonaldo M.F., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.

Brownstein M.J., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

Nichards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.

Niting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska W., Smailus D.E.,

Generation and initial analysis of more than 15,000 full-length

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kalicki J., Elliott G.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: May act as a scaffolding protein involved in the organization of synaptic active zones and in synaptic vesicle trafficking (By similarity).
-!- SUBMIT: Interacts with Rabacl/Pral, RIMS2 and profilin (By similarity).
-!- SUBCELLULAR LOCATION: Concentrated at the presynaptic side of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isold=09%6V0-2; Sequence=VSP_003923, VSP_003925, VSP_003925, VSP_003925, VSP_003925,
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-!- DOMAIN: C2 domain 1 is involved in binding calcium and phospholipids. Calcium binds with low affinity but with high specificity and induces a large conformational change.
-!- SIMILARITY: Contains 2 C2 domains.
-!- SIMILARITY: Contains 1 PDZ/DHR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        synaptic junctions (By similarity).
ALTERMATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=2;
Comment=Additional isoforms seem to exist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP, P04410; 1A25.

Genew; HGNC:13406; PCLO.

MIN, 6.04918; --

GO: 00005856; C:cytoskeleton; NAS.

GO; GO:00058202; C:synaptic junction; ISS.
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The complete sequences of 100 new cr code for large proteins in vitro."; DNA Res. 5:31-39(1998).
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SEQUENCE OF 4405-5147 FROM N.A.
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EMBL, AC004886, AAD21789.1; --
EMBL, BAA25485.1, --
EMBL, BC001304; AAH01304.1; --
EMBL, CC001304; AAH01304.1, --
                                                                                                                                                                   SEQUENCE OF 4405-4439 FROM N.A.
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EMBL; AC004082; AAB97937.1;
PIR; T00634; T00634.
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) KVSSINGETIQTYCVEDTPIC-----FSRCSSLSSLSSLSSAEDEIGCNQTTQE 1295 ADSANTLQIAEIKEKIGTRSAEDPVSBVPAVSQHPRTKSSRLQGSSLSSESARHKAVEFS 1355 VQRVQVLPDADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKDVELRIMPPVQENDNGN 1535 DYEDDK----PINYSERYSEEEQHEEEERPINYSIKYNEEKRHVDQPIDYSLKYATDIPS 1189 SQKOSFSFSKSSSGQSSKTEHMSSSSENTSTPSSNAKRONOLHPSSAOSRSGQPQKAATC 1249 5 SGAKSPSKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPCSGMVS 1415 GIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAA 1475 SDDDDIEILEECIISAMPTKSSRKAK----KPAQTASKLPP---PVARK----PSQLPV 1614 -----YKL------LPSQNRLQPQKHVS-------FTPGDDMPRVY 1642 CVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTDEAQG 1702 GKTSSVT----IPELDDNKAEEGDILAECINSAMPK--GKSHKPFRVKKIMDQVQQASA 1755 SSSAPNKN-----VKP 1778 SKDPPNFNTCTECKNOVCNLCGFNPTPHLTENCQTQRAISGQLGDIRKMPPAPSGPKASP 1039 MPVPTESSSQKTAVPPQVKLVKKQEQEVKTEAEKVILEKVKETLSMEKIPPMVTTDQKQE 1099 KKONLKNNSKDFNDKLP-----NNEDRVRGS-----FAFDSPHHYTPIEG--TPYCF 1856 SRNDSLSSLDFDDDDVDLSREKAELRKA----KENKESEAK---VTSHTELTSNQQSANK 1909 |: | : | | | : | | | : | | TXIIKEQPQPPCTAKPDQEKEDDKSDTSSSQQPKSPQGLSDTGYSSDGISSSLGEIPSLI 1276 9 IPONTEYRIR-----VFSDNKDS 1811 ESKLEKDKASALQEKKPLPEEKKLIPEEKIRSEEKKPLLEEKKP---TPEDKKLLPEAK 1156 -TDE-----KLQNFAIENTPVCFSHNSSLSS-----LSDIDQENNNKENEP--- 1986 1987 -----PQASGYAPKSFHVE 2015 PQEQSRRESINICGITDAPKSQPTTPQETVTCKLFGFGASIFSQASNLISTAGQPGPHSQ 867 : | | : | | : : | | : | | : | | : | | : | | : | | : | | : | | | : | | : | | : | | : | | : | | : | | : | | : | : | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | ---bvqkkee-----bkkaqikmspkdbakempkgspppgprptagquvptqqspk 0 GLOSPAKAPGPTKTPAQTKPPSQQPGSTKPPPQ--QPGPAKPSPQQP-----GSTKPPS 2 AKEWLCIN-COMKRALGGDLAPVPSSPQPKLKTAPVTTTSAVSKSSPQPQQTSPK----K -----NENQEKEAEKTIDSEKDLLDD KTDSAKPSOSFPPTGEKVTPFDSKAIPRPASDSKIISHPGPSSESKGOKQV------TOALAKOPINRGOPKPILOKO-----STFPOSSKDIPDRGAA----ETESEOPKES-----δ

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1836 FEKEPLYGGMLIEDYIYESLVEDTYNGSVDGSLLTRQEEENGFMQQKGREQKIRLSEQIY 1895
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SPEQPKDQEKTQSLSETLEITISEEEIKESQEERKDTFKKDSQQDIPSSKDHKEKSEFVD 1396
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                                                                                                           DIT---TRREPYDSVEESSESE-----NSPVPQRKRRISVGSSSSDBYKQEDSQGSGE
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                                                                     DTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPKKKKFSRL-KGDNEKHSPRNMGGILGE
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QRNEZ4; QBNC02; QRNDF6; QBH9P4; Q9NR13; Q9P222; Q9UDR7;

10.0CT-2003 (Rel. 42, created)

10.0CT-2003 (Rel. 42, Last sequence update)

15.MAR-2004 (Rel. 43, Last annotation update)

Myelioid/lymphoid or mixed-lineage leukemia protein 3 homolog (Histone-lysine N-methyltransferase, H3 lysine-4 specific MLL3) (EC 2.1.1.43)

(Homologous to Alk protein).
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DNA Res. 7:143-150(2000).

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SEQUENCE OF 3193-3865 AND 4460-4911 FROM N.A.

TISSUB=Placenta;

TISSUB=Placenta;

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Wagatsuma M., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara Pakahashi M., Chiba Y., Ishida S., Murakawa K., Ono Y., Takiguchi
                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
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Tan Y.C., Chow V.T.;
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Watanabe S., Kimura K., Murakami K., Ishii S

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-!- DOMAIN: The SET domain interacts with histone H3 but not H2A, H2B and H4, and may have a H3 lyaine specific methylation activity.

-!- MISCELLANEOUS: Found in a critical region of chromosome 7, which is commonly deleted in malignant myeloid disorders. Partial duplication of the MLi3 gene are found in the juxtacentromeric region of chromosomes 1, 2, 13 and 21. Juxtacentromeric region of chromosomes 1, 2, 13 and 21. Juxtacentromeric region of chromosomes 1, 2, 13 and 21. Juxtacentromeric region of chromosomes 1, 2, 13 and 21. SIMILARITY: Contains 1 DHHC-type zinc finger.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 RING-type zinc finger.
-!- SIMILARITY: Contains 1 SET domain.
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Lee J.W.;
Lee J.W.;
Lee J.W.;
Complex that contains a subset of trithorax group proteins.";
Complex that contains a subset of trithorax group proteins.";
Mol. Cell. Biol. 23:140-149(2003).
Cell. Biol. 23:140-149(2003).
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Cell. Biol. 23:140-149(2003).
Cell. Biol. 23:140-149(2003).
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Cell. Biol. 23:140-149(2003).
Cell. Belongs to the ASC-2/NCOA6 complex.
Cell. Subsult: Seadenosyl-L-methionine + histone L.lysine -
Cell. Subsult: Belongs to the ASC-2/NCOA6 complex. (ASCOM), which
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TISSUB=Cervical carcinoma;
MEDLINE=22371496; PubMed=12482969;
GOO Y.-H., Sohn Y.C.,
Kwak E., Barlev N.A., Berger S.L., Chow V.T., Roeder R.G.,
Azorsa D.O., Meltzer P.S., Suh P.-G., Song E.J., Lee K.-J., Lee Y.C.,
Watanabe S., Kimura K., Murakami K., Ishii S., Kawai Y., Saito K., Yamamoto J., Wakamatu A., Nakamura Y., Nagahari K., Masuho Y., Ninomiya K., Iwayanagi T., Iwayanagi T., Iwayanagi T., Iwayanagi T., Wabo human cDNA sequencing project."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                               Duesterhoeft A., Lauber J., Mewes H.-W., Weil B., Wiemarn S., Submitted (JUL-2002) to the EMBL/GenBank/DDBJ databases.
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IsoId=Q8NEZ4-1; Sequence=Displayed;
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SEQUENCE OF 3879-4911 FROM N.A.
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2763 SSSSSSICHSSPSGTVAARVTPFN---YNPSPRKSSADSTSARP----SQIPTPVNNTK 2814

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or send an email to license@isb-sib.cn). EMBL, U19769; AAA82889.1;	398 KRGRREIRVLHL	
ENEL, U2572; ARAGES911;	Db 808 PSERSECR	
PIK; PC4035; PC4035. Genew; HGNC:1857; CENPF. GK; P49454; -	Qy 457 SFDEEHRHAMNELGGLQALAE	SPDEEHRHAMNELGGLQAIAELLQVDCEMYGLTNDHYSITLRRYAGMALTNLFFGDVANK 516
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GO; GO:0005819; C:spindle; TAS. GO; GO:000067; P:DNA replication and chromosome cycle; TAS.	: : 876 SFVAETS	QRISKLQEDTSAHQNVVAETLSALENKEKELQLLNDKVETEQAE 926
GO: GO:0007088; P:regulation of mitosis; TAS. Chromosomal protein; Nuclear protein; Centromere; Coiled coil; Mitosis; Phosphorylation; Antigen; Cell cycle; Repeat; Polymorphism;	Qy 577 LEVKKESTLKSVLSALWNLS.	LEVKKESTLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIES 634 :
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179 SLQTDMTRRQLEYEARQIRVAMEZQLGTC-QDMEKRAQRRIARIQQIEKD	DD 1414 LQSEHKILHDQHCQMSSKMS	 LOSEHKILHDQHCQMSSKMSELQTYVDSLKAENLVLSTNIRNFQGDLVKEMQLGLEEGLV 1473

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Search completed: August 25, 2004, 17:17:17 Job time: 77.5 secs

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Thu Aug 26 06:02:26 2004
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GenCore version 5.1.6 Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - prot	protein search, using sw model	
Run on:	August 25, 2004, 17:05:26; Search time 183.5 Seconds (without alignments) 4888.383 Million cell updates/sec	
Title: Perfect score: 1 Sequence: 1	US-09-442-489F-7 14566 1 MAAASYDQLLKQVBALKMENESSGTQSPKRHSGSYLVTSV 2843	
Scoring table: B	BLOSUM62 Gapop 10.0 , Gapext 0.5	
Searched:	1017041 segs, 315518202 residues	
Total number of h	hits satisfying chosen parameters: 1017041	
Minimum DB seq le Maximum DB seq le	length: 0 length: 2000000000	
Post-processing:	Minimum Match 0% Maximum Match 100% Listing first 45 summaries	
Database : 1 2 2 3 3 3 3 4 4 4 4 4 4 4 4 4 4 4 4 4 4	SPTREMBL 25:* 1: sp_archea:* 2: sp_bacteria:* 4: sp_human:* 5: sp_invertebrate:* 6: sp_mamman:* 7: sp_mnc:* 8: sp_crgaaelle:* 9: sp_phage:* 10: sp_plant:* 11: sp_rodent:* 12: sp_virus:* 13: sp_virus:* 14: sp_unclassified:* 15: sp_archeap:* 16: sp_bacteriap:* 17: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 18: sp_archeap:* 19: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 10: sp_archeap:* 11: sp_archeap:* 12: sp_archeap:* 13: sp_archeap:* 14: sp_archeap:* 15: sp_archeap:* 16: sp_archeap:* 17: sp_archeap:* 18: sp_	
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ALIGNMENTS

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RESULT 1 P70039 PT0039 PRELIMINARY; PRT; 2829 AA.	2,0033; E/3334; 01-FEB-1997 (TrEMBLrel. 01-MAY-1997 (TrEMBLrel.	Last	Xenopus laevis (African clawed frog).	OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;	[1]	-	Submitted (JUL-1996) to the EMBL/	EMBL; U64442; AAB4167	InterPro; IPR008938;	UR INCELTO; LEVOUCES; Armadillo. DR Dfam. DF0614. Armadillo seq. 4	SMART; SM00185; ARM; 5.	SQ SEQUENCE 2829 AA; 310878 MW; 8A2BABDB7706E496 CRC64;	Query Match 72.4%; Score 10544; DB 13; Length 2829;	Si, Conservative 263; Mismatc	KQVEALKMENSNIRQELEDNSNHIJTKI.ETEASNMKEVILKQLQGSIEDEAM	Db 1 MAAASYDQLVKQVEALTMENTNIRQELEDNSNHLIKLETEATNNKEVLKQLQGSIEDEAM 6	OY 61 ASSGOIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 1	INLDSSNIPAGKARPKMSMRSYGSREGSLSGHSGECSPVPVGSFQR	Qy 121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 1	Db 121 KGLINGSRESAGYMEELEKERLLLIAEHEKEEKEKRWYYAQLQNLTKRIDSLPLTENFSM 1

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181 QTDWTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240	181 OTDWTRROLEYBRACIRAAMEEGLGTCODMEKRVOTRVOKIHQIEEEIIRIROLLOSOVA 240 241 E-AERSONKHETGSHDAREROLEOGVOEINMATS-GNOQGSTTRWDHSTASVISSSSTH 298	241 EAAFTPUSHTAGSRDAEKLPDGGTSEITASGNVGSGGGSSSRADHOTTSVNSSTY 300 299 SAPRRITSHLGTKVENVYSLLSMLGTHDKDDMSFTLLAMSSSODSCISMRQSGCLPLLIQ 358	301 SVPRRLTSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCIAMRQSGCLPLLIQ 360 359 LLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGREREIRVLHLEBQIRAYCE 418 361 LLHGNDKDSVLLGNSRGSKEARASGSSAALDNIIHSOPDDKRGREIRVLHLLEDIRAYCE 420	TCWEWQEAHEPGHDODKNPMPAPVEHOLCPAVCYLMKLSFDEEHRHAMNELGGLQAIAEL 47	479 LQVDCEMYGLTNDHYSITLRRYAGMALTNLIFGDVANKATLCSNKGCMRALVAQLKSESE 538	539 DLQQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWNLSAH 598 	599 CTENKADICAVDGALAFLVGTLTYRSQTNTLAIIBSGGGILRNVSSLIATNEDHRQILRE 658	659 NNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMI 718 	719 AMGSAARIRNIMANRPAKYKDANIMSPGSSLPSIHVRKQKALEAELDAQHI.SETFDNIDN 778 	779 LSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSS 836 	837 SRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTSSKR-GLQISTTAAQIAKVMEEVS 895 ::	896 AIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHSNTYNFTKSENSNRTCSMPYAKLE 955	956 YKRSSNDSLANSVGSSDGYGKRGOMKPSIESYSEDDESKFCSYGOYPADLAHKIHSANHMD 1015	1016 DNDGELDTPINYSLKYSDBQLANSGRQSPSQNERWARPKHIIEDBIKQSBQRQSRNQSTTY 1075	1076 PVYTESTDDKHLKFQPHFGQECVSPY-RSRGANGS-ETNRVGSNHGINQNVSQSLCQED 1133 1076 SSYTENKEEKHKKFPPHFNQSENVPAYTRSRGANNQVDQSRVSSNLSNNSKASKPHCQVD 1135	1134 DYEDDKPTNYSERYSEEEQHEEE-ERPTNYSIK-YNESKRHVDQPIDYSLKYATDIPSS- 1190 : :	1191 OKOSFSPSKSSSGOSKTEHMSSSENTSTPSSNAKRONOLHPSSAQSRSGOPOKAAT 1248
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 1308	EKIGTRSAEDPVSEVPAVSQHPRTKSSRLQGSS
1367	RKSPPEHYVQETPLMFSRCTSVSSLDSFESRSIASSVQSEPCS-GMVSGIISPSDLPD 1
1426	GQTMPFSRSKTPPPPPQTAQTKREVPKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDA 1
1486	LHFATESTPDGFSCSSSISALSLDEPFIQKDVELRIMPPVQENDNGNETESEQPKES 1
1546 1548	KRAEKTIDSEKDLLDDSDDDIEILEECIISAMPTKSSRKAKK-PAQTASKLPPP 16
1605	RESQLEVYKLLESQNRLQPQKHVSFTPGDDMPRVXCVEGTPINFSTATSLSDLTIES 1.
1665	AAGEGVRGGAQSGEFEKRDTIPTBGRSTDEAQGGKTSSVTIPELDDNKAEEGDIL 1.
1725	CINSAMPKGKSHKPFRVKKIMDOVQQASASSAPNKNQL-DGKKKKPTSPVKPIPONT 17
 1784	TTRVRKNADSKNNIJAAERVFSDNKDSKKQNLKANSKDFNDKLPNNEDRVRGSFAFDSP 1
1844	PIEGTPYCFSRNDSLSSLDPDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSN 19
σ	NKTGAIAKQPINRGQPKPILQKGSTFPQSSKDIPDRGAATDEKLONFAIENTPVCF 19
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2024	IDSEDDLLQECISS
2082	QRPDSEHGLSPDSENFDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKKSG 214
2142	LGSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKG
2202	SNSEISGQMKQPLQANNPSISRGRTMIHIPGVRNSSSSTSPVSKKGPPLKTPASKSP 2.
2262	TSPRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQPLSRPI
3.2	SPNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGROMSQONLTKQ 23

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                                   Query Match
Best Local Similarity 95.1
Matches 1006, Conservative
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BR PEAM; PRO0514; Armadillo.
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BR PROSITE; PSO0146; ARM REPEAT; I.
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BR ROSITER ROOSE AM; II7633 MM; 86C79FDC12C23FAB CRC64;
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Mus musculus (Mouse).
Bukaryota; Merazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; Musinae; M
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1-MAR-2003 (TIEMBLrel. 23, Last sequence update)
01-OCT-2003 (TIEMBLrel. 25, Last annotation update)
Adenomatosis polyposis coli (Fragment).
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1080 NLDSDSS-----LEGLEEAGPGEAELGRAWRASGSTSLPVS-IPA----PQRGRSR---- 1125
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                             LSALWNLSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIAT
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                                                                        CLPLLIQLLHGNDKDSV---LLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLH
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MEDLINE=99147086; PubMed=10021369;
van Es J.H., Kirkpatrick C., van de Wetering M., Molenaar M.,
Miles A., Kuipers J., Destree O., Peafer M., Clevers H.;
"Identification of APC2, a homoloque of the adenomatous polyposis coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEA--MA
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                                                                                                                                                                                                                                              Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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MGD; MGI:1346022; Apo2.
InterPro; IPR000938; ARM
InterPro; IPR000225; Armadillo.
InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 3.
SMART; SM00164; ARM; 5.
PROSTITE; PS00012; PAOSPHOPANTETHEINE; 1.
SEQUENCE 2274 AA; 243137 NW; 75ABDAISDOF707F5 CRC64;
1021 LDTPINYSLKYSDEQLNSGROSPSQNERWARPKHIIED 1058
1019 LDTPINYSLKYSDEQLNSGROSPSQNERWARPKHVIED 1056
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AJ130783; CAA10207.1; -
AJ130784; CAA10207.1; -
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AJ130787; CAA10207.1;
AJ130788; CAA10207.1;
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                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                Mus musculus (Mouse)
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Db 1948 LAKQHKTQKSPVRIPFMQRPARRVPPPLARPSPEPGSRGRAGAEGTPGARGSRLGLVRMA 1947 Qy 2421 STKSSGSESDRSRPVLVRQSTFIKEAPSTTRRLEESASFESLSPSSRPASPTRSQAQ 2480	RESULT 4 AC 055956 D 065956 PRELIMINARY; PRT; 2303 AA. AC 055966 D 01-MAY-1999 (TERMELTE1 10, Created) DT 01-MAY-1999 (TERMELTE1 10, Last annotation update) DE APCI Droctell. APCI. CO ENGARGACE METAZOA, CATANALES; Last annotation update) CO ENGARGACE METAZOA; CATANALES; Last annotation update) CO ENGARGACE METAZOA; CATANALES; Last annotation update) CO ENGARGACE METAZOA; CATANALES; Last annotation update) CO MOBIL TAXID-9606; PRIMARIA; PRIMATES; CATANTAIN; HOMINIGAE; EMOG. RN NOBIL TAXID-9606; PRIMATES; CATANTAIN; HOMINIGAE; EMOG. RN SEQUENCE FROM N.A. RR SEQUENCE FROM N.A. RR SEQUENCE FROM N.A. RN SEQUENCE FROM N.A. RN SEQUENCE FROM N.A. RN MEDILIFES904066; SP PUBMEd-9823329; RN MEDILIFES904066; D PUBMED-98021329; RN MEDILIFES904066; D PUBMED-98021329; RN MEDILIFES904066; N ANDINED. RN MENEL; ABOZSSS; BAA75499: 1; JOINED. DR EMBL; ABOZSSS; BAA75499:
1341 SLSSESARHKAVEFSSGAKSPSKGAQTPKSPEHYVQETPLMFSRCTSVSSLDSFESRS 1400	1464 DSKKONLÄNNSKDFNDKLPNNEDRVRGSPAPDSPHHYTPIBGTPYCFSRNDSLSSLDFDD 1869 1464 DSSKOTT

999 PAALSLFLGSPFLQGQALARTPPTRRGGKEAEKDTSGEAAVA 840 874 SKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHS- 932		HV	APRRNRGRGLGV SVGSLDSFEGRSIAGS	1180 IPSEPCSGGGSGTISPSELPDSFGQTMPPSRSKIPPLAFAPAPQGPPEATQFSLQ 1232 1463 RESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSLSALSLDEPFIQKD 1519	ISAMPTKSSRKAKKEAQTASKIPPPVARKPSQLPVYKLIPSQNRLQPQKHVSFTPGDDMP	1700 AQGCKTSSYTIPELDDNKAEEGDILAECINSAMPKKSHFFFKVKXIMDQVQAAAASA 1759
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DR GO; GO:0008013; F:beta-catenin binding; TAS. DR GO; GO:000165; P:protain complex assembly; TAS. DR GO; GO:0007165; P:eignal transduction; TAS. DR InterPro; IPR00838; ARM. DR InterPro; IPR001825; Armadillo. DR InterPro; IPR001825; Armadillo. DR Pfam; PF00514; Armadillo.eeg; 3. DR SWART; SM00185; ARM; 5. DR SWART; SM00185; ARM; 5. DR SCOUNCE 2303 AA; 243946 MW; 7BF940183ACD643D CRC64; CQUERY MAtch 23.44; Score 3415.5; DB 4; Length 2303; Best Local Similarity 34.44; Ered. No. 38-159; Matches 997; Conservative 372; Mismatches 815; Indels 717; Gaps 94;	QY 2 AAASYDQLLKQVEALKAENSNILRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEA 59 E	OY 120 RR-GFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPLTE-N 177	2298 3 263 358		Db 439 AVAELLQVDYEMHKYTRDPIALALRRYAGMTLTNLTFGDVANKATLCARRGGMEAIVAQL 498	OY 654 QILRENNCLQTLLQHLKSHSLTIVSNACGTLMNLSARNPKDQEALWDMGAVSMLKNLIHS 713

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annotation
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                            Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                              C STRAINE-22354683; PubMed=12466851;
A The FANTOM Consortium,
The RIKEN Genome Exploration Research Group Phase I & II Team;
The RIKEN Genome Exploration Research Group Phase I & II Team;
Thalysis of the mouse transcriptome based on functional annotation, To (170 full-length colbas.);
I Mature 420:563-573 (2002).;
EMBL; AK045053; BAC32198.1; -.
RGD; GC:0005634; Apc.
GC: GC:0005737; C:Cytoplasm; IDA.
GC: GC:0005634; C:nucleus; IDA.
GC: GC:000613; F:bet-catenin binding; IDA.
GC: GC:0009752; P:anterior/posterior pattern formation; IMP.
GC: GC:0009753; P:axis specification; IMP.
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 polyposis coli
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                                                                                                                                                           EEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMK 2214
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               STPPOSSKDIPDRGAATDEKLQ-NFAIENTPVCFSHNSSLSSLSDIDQENNNKENEPIKE 1989
                                   KEAPAPSKAAP--AAPPPARTQPSLIADETPPCYSLSSSASSLS------EPEP--
                                                                          TEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPK
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QBBRD8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -----AQDRVQQTEPQALLAV-----KSVPVDEDPETEVPTHPED 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   299 SAPRELISHLGTKVEMYYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQ 358
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                                                                                                        MEDLINE=99147086; PubMed=10021369; van de Wetering M., Molenaar M., van Es J.H., Kirkpatrick C., van de Wetering M., Clevers H.; Miles A., Kuipers J., Destree O., Peifer M., Clevers H.; "Identification of APC2, a homologue of the adenomatous polyposis coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SKDSFGELSRATIRLLEELDRERCFLINEIBKEEKEKLWYYSQLQGLSKRLDELPHVETF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YCETCWEWQEAHEPGMD-QDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNELGGLQA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   535 SESEDLOQVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALWN
                                                                                                                                                                                                                                                                                                                                                                                                                     2 AAASYDQLLKQVBALKMENSNLRQELBDNSNHLTKLETBASNMKEVLKQLQGSIBDBA--
                                                                                                                                                                                                                                                                                                                                                                                             53; Gaps
                                   Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo
                                                                                                                                                                                                                                                                                                                                                                     DB 4; Length 733;
                                                                                                                                                                                                      Miles A., Kirkpatrick C., van de Wetering M., Molenaar M., Miles A., Kuipers J., Destree O., Peifer M., Clevers H.; "Adenomatous Polyposis Coli Homologs in Nammals and Flies."; Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AJ012652; CAB61207.1; -. EMBL; AJ012622; AAF01184.1; -. Interpro; IPR000838; ARM. Interpro; IPR000838; ARM Interpro; IPR000825; Armadillo. Pfam, PR0014; Armadillo. Seg; 3. SMART; SM00185; ARM; 5.
                                                                                                                                                                                                                                                                                                                                                                  / Match 14.9%; Score 2170.5; DB 4; Length Local Similarity 57.5%; Pred. No. 1.2e-98; es 445; Conservative 122; Mismatches 154; Indels
                                                                                                                                                                                                                                                                                                                                              80876 MW; 09E56BESF7032BAD CRC64;
                                                                                                                                                           tumour suppressor.";
Curr. Biol. 9:105-108(1999).
protein (Fragment)
                       Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                              733 AA;
                                                                                  SEQUENCE FROM N.A.
TISSUE=Kidney;
                                                                                                                                                                                              SEQUENCE FROM N.A
                                                          NCBI_TaxID=9606;
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RA SEQUENCE FROM N.A.

RA Carr I.M., Markham A.F., Colleta P.L., Wai L., Askham J., Morrison E.,

RA Meredith D.M.;

RI "APC2 alternatively spliced cDNA sequence.";

RI "APC2 alternatively spliced cDNA sequence.";

RI "APC2 alternatively spliced cDNA sequence.";

RI "APC3 alternatively spliced cDNA sequence.";

RI "APC3 alternatively spliced cDNA sequence.";

RI "APC3 alternatively spliced cDNA sequence.";

RI "APC3 alternatively spliced cDNA sequence.";

REMBL, AR110334; AAD28183.1; ---

RO; GO:0005503; P: metalloendopeptidase activity; IEA.

GO; GO:0005503; P: proteolysis and peptidolysis; IEA.

BR O; GO:0005503; P: proteolysis and peptidolysis; IEA.

BR InterPro; IPR001818; Pept M10A.

BR InterPro; IPR001818; Pept M10A M12B.

BR PROSITE; SR00185; ARM3 3.

BR PROSITE; SR00546; CYSTEINE_SWITCH; 1.

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                                                                                                                                                        SVAPYEQLVRQVEALKAENSHLRQELRDNSSHLSKLETETSGMKEVLKHLQGKLEQEARV
595 LSAHCTENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQ
                                    555 ILRENNCLOTLLOHLKSHSLTIVSNACGTLWNLSARNPKDOEALWDMGAVSMLKNLIHSK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            120 RR-GFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENF
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                                                                                                                                                                                                                                               715 HKMIAMGSAAALRNIMANRPAKYK-DANIMSPGSSLPSLHVRKQKALEAELDAQ 767
                                                                                                                                                                                                                                                                             Craniata, Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT; 1246 AA
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
NCBI_TaxID=9606;
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925 SL 1338 QGSSLS	OY 1398 SRSIASSYQSEPCR	OY 1513 EPFIQKDVELRIMPPVQE:	1573 1205 1631 1245	1299 1728 1728 1728 1728	OY 1770 KEPGARAQQMQEQPIVGS: Db 1419 KEPGARAQQMQEQPIVGS: QY 1804 VFSDNKDSK-KQNLKNN- Db 1479ERKDEKILQECINTG ON 1861 SISSLDFDDDDVDLSREK	1524 1919 1578 1964	Db 1637 HKDPDLMLKSVERLTMEF Qy 1996 QGEPSKPQASGYAPKSFH Db 1692 VSFPSVSQTA Qy 2053 PSRLKGDNEKHSPR Qy 2053 PSRLKGDNEKHSPR 1733 PSRLEGETDTLVNGHADS	
: : : :		GMALTNLTFGDVA LMALTNLTFGDEN TLREVGSVKALME		695 QEALWDMGAVSMLKNLIHSKHKMTAMGSAAALRNLMANRPAKYKDANIMSPG-SSL 749	### ##################################	THSNITYNFTKSENSNRTCSMPYAKLEYKRSSNDSLNSVSSSDGYGKRGQMKPSIESYSED	1050 ARPKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSFYRSRGANG 1109	1224 NAKRONOLHPSSAQSRSGQPQKAATCKVSSINOFTIQTYCVEDTPICFSRCSSLS 1278 :
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	925	SLDESGKANQAIVGTDADIKPKLEKQEEQESQPAEQVLTKPPTQANSAL	973
	1338	QGSSLSSESARHKAVEFSSGAKSPSKSGAQTPKSPEHYVQETPLMFSRCTSVSSLDSFE	1397
	974	RS	392
	1398	SRSIASSVQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREV	1452
	993	DVDVANCDDKSSVVSD-FSRLASGVISPSEIPDSPTQSMPQS	1033
	1453	PKNKAPTAEKRESGPKQAAVNAAVQRVQVLPDADTLLHPATESTPDGFSCSSSLSALSLD	1512
		RDRIOKDVELRIMPDVORNONGNETESEOPKESNENOEKE-AEKTID	1558
	60	:	7
	1559	SEKD	1572
	1145	SYCTEDTPALLSKVPSNTNLSVISMSSTDPKDATAGQAQMYAHQLSDDVSSNASDCGGAS	1204
	57	-EILEBCIISAMPTKSSRKAKKPAQTASKLPPPVARK-PSQLPVYKLLPSQNRLQPQKHV	1630
	1203	GREEDGGCIREGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	1686
	2 4	ADEMNK-PLVEDSPCNFSVVSGLSNLTVGSSLVGPAVQLKETE-PSSADQNPEMKR	29
	1687	RDIIPTEGRSTDEAGGGKTSSVTIPELDDNKAEEGDILAEC	1727
	1299	SLANRSKSRRPPHWQDDSLSSLSIDSEDDTNLLSQAIAAGCNRPKSNLGFSSNGKRSSSL	1358
	1728	INSAMPKGKSHKPPRVKKIMDQVQQASASSSAPNKNQLDGKK	1769
	1359	SSSQPIAINAATSASSLNSAMTVRKSQQQESYSSVDSSDSNDNQSKSLFELCILKGMYKT	1418
	1770	KKPTSPVKDIPQNTEYRTRVRKNADSKNNLNAER :	1803
	40 0		1860
	1479	ERKDEKLLQECINTGISKKIN-AVPKNVLATSAALEPCHPWAAT	52
	1861	LSREKAELR	1918
	1524	:	1577
	1919	-NRGOPKDILOKOSTFPQSSKDIPDRGAATDEKLONFAIENTPVCF	1963
	1578	PIQGNGNASQNGLET-ATGSKDLDSEDRSSDESNQSFIMETWVRLDSALNETČISGASEK	1636
	1964	SHUSSTSSTSDDGENNIKENEDIKETEPPDS	1995
	1637	HKDPDLMLKSVERLTMEFVTSAEQLRSSSHNHSSSNSHKNNSSNNTWNESTCPND	1691
	1996	SFHVEDTPVCFSRN	S
_	1692	-	1732
	2053		0 1
	1733	PESLEGETDTLVNGHADSYSGSSGGLNFQLGGQVQNAGVRLEPQRLLFNGTSASIMT	78
	2109		2152
•	1790	NSTMIA	, ,
	2153	DQEEKPFTSNKGPRILKPGEKSTLETKRIESESKGIKGGKKVIKS	189
	1850	SSLRQAMPS-KSPRFARKMFPANLVARRALGHLAG	1

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RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Burtis K.C., Bussam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Durbin K.J., Evangeliste C.C., Ferraz C., Ferriers B., Fleischmann W.,
RA Foeler C., Gabriellan A.E., Garrell J.H., Gu Z., Gaua P., Harris M.,
A Glasser K., Gorger C.C., Ferraz C., Ferriers S., Fleischmann W.,
RA Glock A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
A Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Jalai M., Kalush F., Karpen G.H., Ke Z., Kennison J. A., Ketchum K.A.,
RA Laako P., Lei Y., Levytsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alako P., Lei Y., Levytsky A.A., Li J., Li Z., Liang Y., Lin X.,
Alako P., Lei Y., Levytsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Laako P., Lei Y., Levytsky A.A., Li J., Li Z., Liang Y., Lin X.,
Allshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.,
RA Relazolo M., Pittman G.S., Pan S., Pollatch J., Puri V., Reese M.G.,
RA Relazolo M., Pittman G.S., Pan S., Pollatch J., Smith T.,
Shie B.C., Siden-Kiamos I., Saudeton M., Stupski M.P., Smith T.,
Shie E., Spradling A.C., Stapleton M., Stupski M.P., Smith T.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Milliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA Zheng X.H., Zhong F.N., Zhan M., Zhang G., Zho Q., Zheng L.,
R. Zheng X.H., Zhong F.N., Zhong W., Zhu S., Zhu X., Zhu X., Smith H.O.,
R. Schnece Sequence of Drosophila melanogaster.",
R. Schnece Sequence Of Drosophila melanogaster.",
R. Reiner R. Renning C. L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    243 ERSSQNKHETGSHDAERQN-EGQGVGEINMATSGNGQGSTTR-----MDHETASVLSSS 295
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SSSQDSCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDD 397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    296 STHSAPR------RLISH-----LGTKVEMVYSLLSMLGTHDKDDMSRTLLAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 ELREMREHRSLDRNFERQSAQQQLDELPPRNGGGSPASAGRPSRSKEPSYTLSRFLDGD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               398 KRGRREIRVLHLLEQIRAYCETCWEWQEAHEPGM--DQDKNPMPAPVEHQICPAVCVLMK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        456 LSFDEEHRHAMNELGGLQALAELLQVDCEMYG-LTNDHYSITLRRYAGMALTNLTFGDVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     350 VSFDEEHRHAMCELGALHAIPNLVHLDHAVHGPKPEDQCCNSLRRYALMALTRILFFGDEN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 25.3%; rreq. No. 3.55.7.9; Conservative 325; Migmatches 838; Indels 964;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 2417;
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261282 MW; 08327727C475F254 CRC64;
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                                                     1898 IKPPSLMDELLDSMISVDSIQSEVADGEQDCSMATTISVSNYETAACDDQTMTVLQSCFD 1957
                                                                                                                                                1958 EDEDATMNDYSSÄESTPKKIGSTPSPNRRSLTPKDKRRLTKDRFKTYTIATSCEMBAPEAN 2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----SNNAAPSKKKTLSPIJAKRSLVPGGSGVRLPAKKKPTPPPBPAPARLERQGTF 2230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2504 WRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWKREHSKHSSSLPRVST 2563
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Eukaryota, Metazoa, Arthropoda, Hexapoda, Insecta, Pterygota,
Booptera, Endopterrygota, Diptera, Brachycera, Muscomorpha,
Ephydroidea, Drosophilidae, Drosophila.
                          MKQP----LQANMPSISRGRIMIHIPGVRNSSSSTSPVSKKGPPL-
                                                                                                                                                                                                                                                                                                                                                                                                 2138 DLRTSVVKPTTLEPATAVKLVRGRKKPAYVSPYSMQSQRN-----
                                                                                                                                                                                        QTSQI----GGSSKAPSRSGSRDSTPSRPAQQPLSRPI---
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01-WAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
                                                                                                          ------KTPASKSPSEGQTATTSPRGAKPSVKSEL-
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APC OR CG1451.
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1685	EKRDTIPTEGRSTDEAQGGKTSSVTIPELDDNKAEEGDILAEC1727
1298	: : KAKPGKQEQVRRPPHWQDDSLSSLSIDSEDDTNLLSQAIAAGCNRPKSNLGFSSNGKRSS 1357
1728	INSAMPKGKSHKPFRVKKIMDQVQQASASSSAPNKNQLDG 1767
1358	SLSSSQPIAINAATSASSLNSAMTVRKSQQDESYSSVDSSDSNDNQSKSLFELCILKGMY 1417
1768	180
1418	147
1802	ERVFSDNKDSK-KONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSR 1858
1859	KENKESEAKVŢSHŢ
1524	- TSASALSTAAPDV
1919	FPQSSKDIPDRGAATDEKLONFAIEN 195
1564	DAIATVTDTVRSPAAPNQGNGNASQNGLET-ATGSKDLDSEDRSSDESNQSFIMETMVRL 1622
1959	SLSDIDQENN 198
1623	NSHKN 167
1981	NKENEDIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDD 2037
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2038	E 177
2094	PDSENPDWKAIQEGANSIVSSLHQAAAAACLSRQASSDSDSILSLKS 2140
1776	PORLLFNGTSASIMTNSTMIAFEARALAENLOPAATDDDTTEMTFSLNSLDLDNIRPPS 1835
2141	SLGSPFHLTPDQEEKPFTSNKGPRILKPGEKSTLETKKIESESKQIKGGKKVYKS 219
.1836	β Α Τ
2198	SEISGQMKQPLQANMPSISRGRTMIHIPGVRNSSSSTSPVSKKGPP 225
1885	VSNYETA 194
2253	TPASKSPSEGQTATTSPRGAKPSVKSEL
1944	꿆
2283	232
2004	YTIATSCEMEAPEANETLQIBIVEAAVPVATPSPRANGRRRGSAERYKTQLIBCPLALIQ 206
2322	QSPGRNSISPGR 233
2064	PQPDDCPSEQLSSIRAMMQQFTFITDINIGHSQETCESTDHPEDAGESPECDQNSETESC 2123
2334	NGISPPNKLSQLPRIESPSTASIKSSGGKMSYTSPGRQMSQONLIKOT 2382
1717	
2383	GLSKNASSIPRSESASKGLNOMMNGAGANKKVELSKASIKASGSESJKRSEFFV 23-3- 1
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FWK 2548 : R 2289	/SA 2608 : 1QS 2349	IED 2663 2397				coli			86;		ET 772 : QA 120	817 AS 180	TS 873 : :VA 222	S- 932
2489 PDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTWK	2549 REHSKHSSSLPRVSTWRRTGSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVSA 2290 RMTPQRANTSLRLAAGKSHAASRVVSGRVSSTTPPSRSNSNLNGSSAAAAAAKINHAQS	2609 KGTWRKIKENEFSPTNSTSQTVSSGATNGAESKTLIYQMAFAVSKTEDVWYRIED :	2664 CPINNPRSGRSFTGNTPPVIDSVSEK 2689 2398NTPSTAGGVKSK 2409	LT 10 QUEMB PRELIMINARY; PRT; 1685 AA. QOUEMB; 01-MAY-2000 (TrEMBLrel. 13, Created) 01-OCT-2003 (TrEMBLrel. 13, Last sequence update) APC2 protein (Fragment).	APC2. Homo sapiens (Human). Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;	J GUBNCE FROM N.A. DLINE=99147086; PubMed=10021369; N B. J.H., Kirkpatrick C., van de Wetering M., Molenaar M., Les A., Kuipers J., Destree O., Peifer M., Clevers H.; dentification of APC2, a homologue of the adenomatous polyposis	KT tumour suppressor."; RL Curr. Biol. 9:105-108(1999). DR GD; AJJ31187; CAAL0317.1; DR GO; GO:0005578; C:extracellular matrix; IEA. DR GO; GO:0006508; P:metalloendopeptidase activity; IEA. DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA. DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.	INTERING TRANSCASS, ARM: INTERING TRANSCASS, ARM: INTERING TRANSCASS, ARM: INTERING TRANSCASS, ARM: INTERING TRANSCASS, ARM: INDA TER INDA	Similarity 28.5%; Pred. No. 2.9e-75; 1; Conservative 263; Mismatches 664; Indels 682; Gap	654 QILRENNCLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHS	714 KHKMIAMGSAAALKNLMANRPAKYK-DANIMSPGSSLPSLHVRKQKALEAELDAQHLSET 	773 FDNIDNLSPKASHRSKQRHKQSLYGDYVFDTNRHDDNRSDNFNTG ::::	818NYTVLSPYLNTTVLPSSSSRGSLDSSRSEKDRSLERERGIGLGNYHPATENPGTS :	874 SKRGLQISTTAAQIAKVMEEVSAIHTSQEDRSSGSTTELHCVTDERNALRRSSAAHTHS- : :: :
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112 THRAUGSHIGTHONNOGGELOGEDDYPDINPERNYSERVEEDGHEERERPHYNEIKNBERR HTT. 134	34	PKHIIEDEIKQSEQRQSRNQSTTYPVYTESTDDKHLKFQPHFGQQECVSFYRSRGANGS	Ч 4
1.12 HYDOPIDYSLKXATDIPSGOCGERSEASSGOSKTEHWSSSSENTSTFSDANUM. 1.3 1.39 HYDOPIDYSLKXATDIPSGOCGERSEASSGOSKTEHWSSSSENTSTFSCANCE, 1.3 1.30 HYDOPIDYSLKXATDIPSGOCGERSEASSGOSKTEHWSSSSENTSTFSCANCE, 1.3 1.31 HYDOPIDYSLKXATDIPSGOCGERSEASSGOSKTEHWSSSSENTSTFSCANCE, 1.3 1.32 HYDOPIDYSLKXATDIPSGOCGERSEASSGOSKTEHWSSSSENTSTFSCANCE, 1.4 1.33 HYDOPIDYSLKYPEXILAAAPL-SVASKALOKTAAACGEGISLSRCSILSSLSSA-GREGERS 1.4 1.44PADHILSKYPEXILAAAPL-SVASKALOKTAAACGEGISLSRCSILSSLSSA-GREGERS 1.4 1.45PADHILSKYPEXILAAAPL-SVASKALOKTAAACGEGISLSRCSILSSLSSA-GREGERS 1.4 1.46 GODIDDDDSSLGGLEAPSGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG	11	TNRVGSNHGINQNVSQSLCQEDDYEDDKPTNYSERYSEBEQHEBEERRPINYSIKYNEEK	-
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414PADHLEKVPERATCKYSSINOETIGYTVCVEDTPICFGRCSSISSISSABEDEIGGWO 129 415PADHLEKVPERALABAPL-SVASKALGKLAAGEGPLSISRCSSISSISSAGRGFSE 468 4292 TTOEADSANTLOIALIKAAAPL-SVASKALGKLAGEGPLSISRCSSISSISSAS 134 469 GGDLDDSDSSLEGLEEAGPSEÄELDSTWRAPGATSLPVAIPAPRRAKGRGLG 520 3145 SARHKAVEPSSGAKSPEKSAGAPTSPEHVYOETPLMFSRCTGVSSLDSFESPSIASS 140 521	17 38	HVDQPIDYSLKYATDIPSSQKQSFSFSKSSGQSSKTEHMSSSSENTSTPR	12 41
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10	41	PADHLSKVPEKLAAAPL-SVASKALQKLAAQEGPLSLSRCSSLSSA-GRPGPS	SO.
SARHKAVEFSGGAKSPEKSGAQTPKSPPEHYVQETPLMFSRCTSVSSLDSFESRSASS 140	46	TYGEADSANTLGIAEIKEKIGTRSAEDPVGEVPAVSOHPYTKSSRLOGSSLS GGDLDDSDSSSLEGLEEAGPSEAELDSTWRAPGATSLPVAIPAPRRNRGRGLG	(A)
405 VQSEPCSGWVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAGTKREVPKXARPTARK 146 51 1FSEPCSGGVSGTISPSDLPDSPGQTMPPSRSKTPPPPPQTAGTKREVPKXARPTARK 146 52 IFSEPCSGGGSGTISPSELPDSPGQTMPPSRSKTPPLAPAPGGGPPEATQFSLO 614 53 RESGRPCAAAVANORVOVLDADTLLHPATESTPDGFSCGSSLSALSLBEPFTQKD 151 615 WESYVKRFLDIADGRERCRLPSELDAGS-VRFTVEKPDENFSCASSLSALALHEHYVQQD 673 520 VELRIMPPVQENDNGNETESBQPKESNBNQEKEAEKTIDSEKDLLDDSDDDIEILEBGT 179 530 VELRIMPPVQENDNGNETESBQPKESNBNQEKEAEKTIDSEKDLLDDSDDDIEILEBGT 179 540 VELKLLPSACPERGGAGAGLHPAGHRREEGPAPTGSRPRGAADQELEILERGC 179 551	3.4	ESARHKAVEFSSGAKSPSKSGAQTPKSPEHYVQETPLMFSRCTSVSSLDSFESRSIAS	ò
405 VQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPKXMAPTARE 146 1	N	VGDATPSSSSENYVQETPLVLSRCSSVSLGSFESPSIAS	9
463 RESGPKQAAVNAAVQRVOULPDADTLLHFATESTPDGFSCSSSLSALSLDEPFIQKD 151 [1]	4 0 5 6	VQSEPCSGMVSGIISPSDLPDSPGQTMPPSRSKTPPPPPQTAQTKREVPKNKAPTA :	146
	46	RESGPKQAAVNAAVQRVQVLPDADTLLHFATESTPDGFSCSSS 	151
	0 5	VELRIMPPVQENDNGNETESEQPKESNENQEKEAEKTIDS : :	57
	α	ISAMPTKSSRKAKKPAQTASKLPPPVARKPSQLPVYKLLPSQNRLQPQKHVSFTPG	63
640 RVYCVEGTPINFSTATSLSDLTIESPPNELAAGEGVRGCAQSGEFEKRDTIPTEGRSTDE 169 771 CTDSABGTPVNPSSAASLSDETLGGPPRDQPGGPAGR	'n		7
700 AQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKGKSHKPFRVKKIMDQVQQASASSSS 175 818 RQA	4 6	RVYCVEGTPINKSTATSLSDLTIESPPNELAAGEGVRGGAQSGEFEKRDTIPTEGRSTD	17
818 RQA	70	AQGGKTSSVTIPELDDNKAEEGDILAECINSAMPKCKSHKPFRVKKIMDQVQQASASS.	75
760 PNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVFSDNKD 181	\vdash	RQAAGHRHKAGHRHK	3
### ### ### ### ### ### ### ### ### ##	16	PNKNQLDGKKKKPTSPVKPIPQNTEYRTRVRKNADSKNNLNAERVF	81
### SKKONLKNNSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDFDDD 187 ###################################	m	SEQSRGAGKNRAGLELPLGRPPSAPA	9
931 DVDLSREKAELRKAKENKESEAKVYSHTELTSNQOSANKTQALAKQPINRGQPKPILQKQ 193 997	81	SKKONLKANSKDFNDKLPNNEDRVRGSFAFDSPHHYTPIEGTPYCFSRNDSLSSLDF GEFD	87
1	0 0	GONEG	ם ו
931 STFPQSSKDIPDRGAATDEKLQ-NFALENTPVCFSHNSSLSSLSDIDQENNNKENEPIKE 1981 	9 6	UVULSKEKAELKRAKRIKESEKAVISHTELISNQOSAKTQALAKQPINRQQPKPIL DEEPPAAAPTPTHRRTSALPR-AFTRER	2 3
28 KEAPAPSKAAPAAPPPARTQPSLIADETPPCYSLSSSASSLS97	93	TFPQSSKDIPDRGAATDEKLQ-NFAIENTPVCFSHNSSLSSLSDIDQENNNKENEE	00
	C/I	KEAPAPSKAAPAAPPPARTQPSLIADETPPCYSLSSSASSLSEPE	7

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EAERSSOSRHDAASHEAGRQHEGHGVAESNTAASSSGQ 276
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                                                                                                                                                                                                   8.6%; Score 1252; DB 11;
31.4%; Pred. No. 6.1e-54;
ive 8; Mismatches 14;
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Last sequence update)
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                                                                                                                                                                                                                          Best Local Similarity 91.4%;
Matches 254; Conservative
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01-NOV-1999 (TrEMBLrel. 12,
01-OCT-2003 (TrEMBLrel. 25,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APC2 protein.
APC2 OR E-APC OR CG6193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EEVAAPKTNSSTSPSLETREPP-----GAPVG--GQL 1605
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1606 SLİGS--DVDGPSLA------KAPIS-----APFVHEGLGVAVGGFPASRH 1643
                                                                      2098
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                                                                                                                                         2154
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                                                                                                                                                                                                            EEKPFTSNKGPRILKPGEKSTLETKKIESESKGIKGGKKVYKSLITGKVRSNSEISGQMK 2214
   TEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQECISSAMPK 2049
                                                                                                                                                                                                                                                                                                             QKTTPGVPAVLRGRIVIYVPSPAPRAQPKGTPGPRATPRKVAP-----PCLAQPAAPAKV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2548 KREHSKHSSSLPRVSTWRRTGSSSSILSASSESSEKAKSEDEKHVNSISGTKQSKENQVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --LSPDSEN
                                                                                             1066 VEWRAIQEGANSIVTWIHQAAA---TREASSESDSILSFVSGLSVGSTLQPPKHRKGRQ
                                                                                                                                                                                                                                              1123 AEGEMGSARRP-----EKRGAASVKTSGSPRSPAGPEK------PRGT
                                                                                                                                                                                                                                                                                   QPLQANMPSISRGRIMIHI------SKS
                                                                                                                                                                                                                                                                                                                                                      PSEGQTATTS-PRGAKPSVKSELSPVARQTSQIGGSSKAPSRSGSRDSTPSRPAQQPLSR
                                                                                                                                                                                                                                                                                                                                                                                        215 PSPGQQRSRSLHRPAKTSELATLSQPPRSATPPARLAKTPSSSSGTS----PASQPLPR
                                                                                                                                                                                                                                                                                                                                                                                                                         ---PIQSPGRNSISPGRNGISPPNKLSQLPRTSSPSTASTKSSGSGKMSYTSPGRQMSQQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2377 NLTKQTGLSKNASSIPRSESASKGLNOMNKONGA-NKKVELSRMSSTKSSGSESDRSERP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1317 RPARR-GPPPLARAVP--EPGPRGRAGTEAGPGARGGRLGLVRVASALSSGSES--SDRS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2496 HSSVQ------AGGWRKLPPNLSPTIEYNDGRPAKRHDIARSHSESPSRLPINRSGTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2720 NRINSFIQVDAPDQKGTEIKPGQNNPVPVSETNESSIVERTPF-----SSSSSSKH
                                                                                                                                         2099 FDWKAIQEGANSIVSSIHQAAAAACLSRQASSDSDSILSLKSGISLGS----PFHLTPDQ
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus
NCBI TaxID=10090;
                                                                      1050 KKKP-SRLKGDNEKHSPRNMGGILGEDLTLDLKDIORP---DSEHG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Adenomatosis polyposis coli.
Mus musculus (Mouse).
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MEDLINE=20196066; PubMed=10731132;
Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
Adams M.D., Celniker S.E., Holt R.A., Floskins R.A., Galle R.F.,
Amanatides P.G. Scherer S.E., Holt R.A., Hoskins R.A., Galle R.F.,
Cocy R.A., Ewis S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
Brandon R.C., Nogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
April J.F., Agbayran A., An H.-J., Andrews Ffannkoch C., Baddwin D.,
Ballew R.M., Basu A., Baxendale J., Bayrakkaroglu L., Beasley E.M.,
Ballew R.M., Basu A., Baxendale J., Brokstein D., Bolshakov S.,
Ballew R.M., Buck J., Brokstein D., Bolshakov S.,
Burkis K.C., Busam D.A., Buller H., Cadieu E., Center A., Chandra I.,
Abrika K.C., Busam D.A., Bulle C., Davenport L.B., Davies P.,
Achier J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
Ab Dodson K., Doug L.E., Downes M., Diagan-Rocha S., Dunkov B.C., Dunn P.,
Achiel M., Gangelista C.C., Ferriaz C., Ferriara S., Fleischmann W.,
Roldek A., Gong F., Garlell J.H., Gu Z., Ganan P., Harris M.,
Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J., 2; ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 120 118 180 RIFVNGSRESTGYLEELEKERSLILADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 178 240 9 09 SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUB=Cerebellum;
STRAIN=CS7BL/6J; TISSUB=Cerebellum;
STRAIN=223564831; PubMed=12466851;
The FANTOM Consortium,
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I of II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
the RIKEN Genome Exploration Research Group Phase I & II Team;
stalls for the mouse transcriptome based on functional annotation of 60,770 full-length cDNs.";
Nature 420:53-573 (2002).
EMBL; AK082724; BAC38587.1; -.
SEQUENCE 324 AA; 36909 MW; D74E29ECD952DICC CRC64; OTDMTRROLEYEAROIRAAMEEOLGTCODMEKRAORRIARIQOIEKDILRVROLLOSOAA QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 1 MAAASYDQLLKQVEALKMENSNIRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDETM 121 RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM Gaps 2; Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endoptera; Diptera; Brachycera; Muscomorpha; Ephydroidea; Drosophilidae; Drosophila. Indels

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A Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C., Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A., A Manel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z., Lang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Liang Y., Lin Z., Mattei B., McIntosh T.C., McDeed M.P., Morris J., Mohrerson D., A. Melson E.M., Moy M., Murphy B., Murphy L., Murphy D., Morris J., Moscon D.L., R. Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M., A. Palazzolo M., Pittman G.S., Pan S., Polland J., Phuri V., Reese M.G., Rhenert K., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T., Spier E., Spradling A.C., Linner R., Wenisenbach J., Wang X., Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J., Wang X., Walliams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Zhao W. J., Yeh R. P., Zaveri J.S., Zhan M., Zhou X., Zhu S., Zhu X., Smith H.O., R. Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., R. Zhence 2877:2185-2195(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yu X., Bienz M.;
"A new Drosophila APC homolog concentrated in apical adhesion zones of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           329 DMSRTLLAMSSSQDSCISMRQSGCLPLLIQLLHGNDKDSVLLGNSRGSKEARARASAALH
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InterPro; IPR008938; ARM.
InterPro; IPR00825; Armadillo.
Pfam; PF00514; Armadillo.seg; 4.
SMART; SM00185, ARM; 6.
PROSITE; PS50176; ARM REPEAT; 1.
SEQUENCE 1067 AA; Il6702 MW; 20C8F5F6121888F8 CRC64;
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EMBL: AAE063746; AAE56249.1; -.
EMBL: AFF113913; AAD50227.1; -.
EMBL: AF091430; AAD20985.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  epithelial cells.";
Nat. Cell Biol. 0:0-0(1999)
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Curr. Biol. 9:105-10
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SEQUENCE FROM N.A.
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q	os S	ço G	Q QD	ે ત	8 8	g &	6 8 7	7 A	P O	ço Db	<i>≿</i> 8	QY Gb	\text{S} 43	که م م	දු පු	S S	& B	\$ 65	ζ.
	QY 1787 TRVRKNADSKNNLNAERVFSDNKDSKKQNLKONSKDFNDKLPNNEDRVRGSFAFDSPHHY 1846 DD 965STSSSLANASTSTLCRENGQSKKQVEHGDK-PN 996	QY 1847 TPIEGTPYCFSRNDSLSSLDFDDDDVDLSREKAELRKAKENKESEA 1892	QY 1893 - KVTSHTELTSNQ 1904 ::::	13	180 Q96180 PRELIMINARY;	DT 01-DEC-2001 (TEMBLET. 19, Created) DT 01-DEC-2001 (TEMBLET. 19, Last sequence update) DT 01-OCT-2003 (TEEMBLET. 25, Last annotation update)			[1] SEQUENCE FROM N.A. SEQUENCE FROM N.A. STARIN-Berkeley; STARIN-Berkeley; Starleton M., Brokstein P., Hong L., Aqbayani A., Carlson J			DR InterPro; IPR00225; Armadillo. DR Pfam; PF00514; Armadillo_seg; 4. DR SMART; SM00185; ARM; 7. DR PROSTUR: PS50176; ARM REPEAT. 1.	SEQUENCE 1067 AA; I16678 MW; 03C4119AEF1 Query Match 8.4%; Score 1221.5; Best Local Similarity 26.3%; Pred. No. 9.7e-	9; Indels 647; Gaps SSVLLGNSRGSKEARARASAALH	уасоасн аруеноі	63 MIVHNNPEEKERQREVKMLRLIDQILDYCNFLHTQLQSGGEALADDEDRHPL 447 CPAVCVLMKLSFDEEHRHAMNELGGLQAIAELLQVDCENXG-LTNDHYSITLRRYAGWAL ::	- AAMKLIMKASFDEEHROTMCELGALKAIPNLVHLDHAVHGPAAGMEQCNALRSYGLMAL. TNLTFGDVANKATLCSMKGCMRALVAQLKSESEDLQQVIASVLRNLSWRADVNSKKTL : : :	Db 174 TWITFGDENVHNKSYLCGQRQFMEVVIAQIATAPDELLQVLAGVLRGWRADKHMKTIF 233 Qy 564 REVGSVKALMECALEVKKESTLKSVLSALWNLSAHCTENKADICAVDGALAFLVGTLTYR 623	Db 234 NELGTVISLARAAMONKNENTLKAILSALWNLSAHCSTNKAEFCAVDGALAFLVGMLSYE 293 Oy 624 SQINILAIIESGGGILRNVSSLIATNEDHRQILRENNCLQIILQHLKSHSLIIVSNACGI 683

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                                                                                                                     1847 TPIEGTPYCFSRNDSLSSLDFDDDDVDLSREK-----AELRKAKENKESEA----- 1892
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-----GSAKAGPVLK---LPM--RTAEEAQA------PKLPPRRSAVQGD-----AEP 924
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                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. MEDLINE=20435068; PubMed=10982189; Su L.K., Steinbach G., Sawyer J.C., Hindi M., Ward P.A., Lynch P.M.; "Genomic rearrangements of the APC tumor-suppressor gene in familial
                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Adenomatosis polyposis coli tumor suppressor (Fragment).
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208 AA; 22726 MW; 51076F257B61C528 CRC64;
                                              925 RLPPKKSDSLSSLSMDSDDDCNLLSQAIAAGSC-
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Hum. Genet. 106:101-107(2000).

EMBL; AF127506; AAF34355.1; -.

EMBL; AF127034; AAF34355.1; JOINED.
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InterPro; IPR000225; Armadillo.
Pfam; PF00514; Armadillo_seg; 2.
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MEDLINE=22388257 PubMed=12477932;

MEDLINE=22388257 PubMed=12477932;

Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

A Riabsner R.D., Collins F.S., Wagner L., Schaefer C.P., Bhat N.K.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,

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Bolatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McKwan P.J., McKernan K.J., Mallek J.A., Gunzarane P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Boninger A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Jones S.J., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
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EUKATOOLA; Metazona; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.
EMBL; BC056268; AAH56268.1; -
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01-OCT-2003 (TrEMBLrel. 25, Created)
01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Hypothetical protein (Fragment).
Homo sapiens (Human).
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Best Local Similarity 98.7
Matches 153, Conservative
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completed: August 25, 2004, 17:23:07 He : 214.5 secs

159 AA

PRT;

PRELIMINARY;

Q7Z2Q8 Q7Z2Q8;

RESULT 15 Q7Z2Q8 ID Q7Z2Q AC Q7Z2Q

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on:

August 25, 2004, 16:58:01; Search time 180.5 Seconds (without alignments) 4450.319 Million cell updates/sec

US-09-442-489F-7 14566 1 MAAASYDQLLKQVEALKMEN.......ESSGTQSPKRHSGSYLVTSV 2843 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

1586107 seqs, 282547505 residues Searched:

Total number of hits satisfying chosen parameters:

1586107

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES Re

	Description	Aaw76140 Human APC		11	5 Human	321 Human	2782	304	508	896	922	w	Aar26052 APC gene	Aaw35392 Human ade	Aaw38370 Human ade	Abg90964 Human ade	Aar63507 Adenomato	Aar58634 Adenomato	Aab23012 Human APC	Ade56175 Rat Prote	Abg71106 Human ade			Abg09335 Novel hum	Abr58648 Human can	Aay92061 Human APC
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This sequence represents a human familial adenomatous polyposis coli

Aay92060 Murine AP	Abb58126 Drosophil	Aar88353 Mutant A-	Abb62156 Drosophil	Aau37120 Staphyloc	Abb68397 Drosophil	Abb67502 Drosophil	Abb66878 Drosophil	Abul6000 Protein e	Abm72734 Staphyloc		Abj18914 Pathogen		Aaw33894 Flea sali	Aaw82368 Flea sali	Abp39618 Staphyloc	Abb60327 Drosophil	Abb60291 Drosophil	Abb65772 Drosophil	Abb71160 Drosophil
AAY92060	ABB58126	AAR88353	ABB62156	AAU37120	ABB68397	ABB67502	ABB66878	ABU16000	ABM72734	ABP56876	ABJ18914	AAB50654	AAW33894	AAW82368	ABP39618	ABB60327	ABB60291	ABB65772	ABB71160
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1773.5	1765	1490	1222.5	562.5	537	527.5	517.5	517	516	516	515	511.5	507.5	507.5	502.5	492	478.5	474	474
56	27	58	5	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Familial adenomatous polyposis coli, APC; tumour suppressor; therapy; chromosome 5q21; tumourigenesis; retinoblastoma; colorectal tumour; FAP; Gardner's Syndrome; GS; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                             Adenomatous polyposis coli protein - useful in the treatment of cancers associated with mutation(s) on human chromosome 5q21.
                                                                                                                                                                                                                                                                                                                                                                      White RL;
Albertsen H;
                                                                                                                                                                                                                                                                                                                                                                     Kinzler K, Joslyn G, Markham AF, Carlson M,
Thliveris A, Groden J, Anand R, Nakamura Y,
Vogelstein B, Hedge PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Col 41-54; 102pp; English.
                    AAW76140 standard; protein; 2843 AA
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91GB-0000963.
91GB-0000974.
91GB-0000975.
91US-00741940.
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(UYJO) UNIV JOHNS HOPKINS.
(UTAH) UNIV UTAH.
(ZENE) ZENECA PHARM.
                                                             (revised)
(first entry)
                                                                                            Human APC protein #1.
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N-PSDB; AAV56447.
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16-JAN-1991;
16-JAN-1991;
16-JAN-1991;
08-AUG-1991;
12-AUG-1994;
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                                                             25-MAR-2003
23-NOV-1998
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the coling protein from clone DP2.5. The gene for the protein is present on thuman chromosome 5q21 and is also referred to as adenomatous polyposis colingene. It is a tumour suppressor gene, and mutations in this gene that be associated with tumourigenesis in retinoblatome and colorectal tumours, and especially familial adenomatous polyposis (FAP) and colorectal colorectal protein and the nucleic acids can be used in therapy. The nucleic acids that encode them can also be used as probes and primers in detection of the cancers and predisposition to it. (Updated on 25-MAR-2003 to correct PR field.)	Query Match 100.0%; Score 14566; DB 2; Length 2843; Best Local Similarity 100.0%; Pred. No. 0; Matches 2843; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	y 1 maaasydollkquealkmensnirqelednsnhijkteteasnmkevikqlqqsiedeam 60 	QY 61 ASSGQIDELERLKELMLDSSNFPGVKLRSKMSLRSYGSREGSVSSKSGECSPVPMGSFPR 120	QY 121 RGFVNGSRESTGYLBELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL 180	Qy 181 QTDWTRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT 240	QY 241 EAERSSQNKHETGSHDAERQNGGGGVGEINWATSGNGGGSTTRWDHETASVLSSSSTHSA 300	QY 301 PRRITSHLGTKVEMYYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 360	Qy 361 HGNDKDSVLLGNSRGSKEARARAGALHNI IHSQPDDKRGRREIRVLHLLEQIRAYCETC 420	QY 421 WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLWKLSFDEEHRHAMNBLGGLQBIAELLQ 480 DD 421 WEWQEAHEPGMDQDKNPMPAPVEHQICPAVCVLMKLSFDEEHRHAMNBLGGLQBIAELLQ 480	QY 481 VDCEMYGLTNDHYSITLRRYAGMALTNLTFGDVANKATLCSMKGCYRALVAQLKSESEDL 540	OY 541 OOVIASVLRNLSWRADVNSKKTLREVGSVKALMECALEVKKESTLKSVLSALMNLSAHCT 600	Qy 601 ENKADICAVDGALAFLVGTLTYRSQTNTLAIIESGGGILRNVSSLIATNEDHRQILRENN 660	OY 661 CLQTLLQHLKSHSLTIVSNACGTLWNLSARNPKDQEALWDMGAVSMLKNLIHSKHKMIAM 720	Qy 721 GSAAALRNIMANRPAKYXDANIMSPGSSLPSLHVRKQKALEAELDAQHLSETFDNIDNLS 780	OY 781 PKASHRSKORHKOSLYGDYVPDTNRHDDNRSDNFNTGNMTVLSPYLNTTVLPSSSSRGS 840 	
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ු දුරු	961	DGYGKRGQMKPSIESYSEDDESKFCSYGQYPADLAHKIHSANHMDDNDGE 102
oy Qu	1021	SQLNSGRQSPSQNERWARPKHIIEDEIKQSBORQSRNQSTTYPVYTE 108
රු සි	1081	/SPYRS
දු පු	1141	BRPTNYSIKYNEEKRHVDQPIDYSLKYATD
ò a	1201	SENTSTPSSNAKRQNQLHPSSAQSRS
yo da	1261	SLSSAEDEIGCNQTTQEADSANTI
ò a	1321	RLQGSSLSSESARHKAVEFSSGP
& 8	1381	SFE SFE
ço G	1441	VPROKAPTAEKRESGPKQAAVRAAVQRVOVLPD VPKNKAPTAEKRESGPKQAAVRAAVQRVOVLPD
δ Q	1501	SSSLSALSLDEPPIQKDVELRIMPPVQENDNGNETES
Qy	1561	LDDSDDDDIEILEECIISAMPTKSSRKAKKPAQTASKLP
රු දු	1621	DDMPRVYCVBGTPINFSTATSLSDLTIE
ço O	1681	tegrstdeagggktssvtipelddnkaeegdila
çy qa		RVKKIMDOVQQASASSSAPNKAQLDGKKKKPTSPVKPIPONTEYRTRVRKNADSKANLN 1
<u>ک</u> و	1801	CKONLKNNSKDFNDKLPNNEDRVRGSFAF
δ, dg	1861	PDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSA
λŏ	o	QPKPILQKQSTFPQSSKDIPDRGAATDEKLQNFAIENTPVCFSHNSSLSSLSDIDQ

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This sequence represents a human familial adenomatous polyposis coli (APC) protein isolated from 87 cDNA clones. The gene for the protein is present on human chromosome 5q21 and is also referred to as adenomatous polyposis coli gene. It is a tumour suppressor gene, and mutations in this gene have been associated with tumourigenesis in retinoblastoma and colorectal tumours, and especially familial adenomatous polyposis (FAP) and Gardner's Syndrome (GS). The protein can be used in therapy to replace lack of native functional protein and the nucleic acids can be used for gene therapy. The nucleic acids that encode them can also be used as probes and primers in detection of the cancers and predisposition to it. (Updated on 25-MAR-2003 to correct PR field.)
                                     Familial adenomatous polyposis coli, APC, tumour suppressor, therapy, chromosome 5q21, tumourigenesis, retinoblastoma, colorectal tumour, FAP, Gardner's Syndrome, GS; predisposition.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cancers
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R, Nakamura Y,
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100.0%; Score 14566;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2843; Conservative 0; Mismatches
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Thliveris A, Groden J, Anand
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      Human APC protein
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16-JAN-1991;
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NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ
                                                                  NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ
                                                                                                                                 ECISSAMPKKKKPSRLKGDNEKHSPRNMGGILGEDLTLDLKDIQRPDSEHGLSPDSENFD
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                                 SFESLSPSSRPASPTRSQAQIPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEVNDG
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  SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG
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The invention relates to a novel method for detecting Adenomatous

C Polyposis Coli (APC) protein in a sample. The method involves contacting

the sample with antibodies which specifically binds to the 2843 amino

acid form of the human APC protein, or to a mutant APC protein, and

detecting an APC-antibody complex. Mutations in the APC grane play a role

c in tumoridenesis, indicating that it is a tumour suppressor gene. It is

located on chromosome 5q21, which corresponds to the PAP (familial)

adenomatous polyposis) locus. FAP is an autosomal dominant inherited

disease in which affected individuals develop hundreds to thousands of

adenomatous polyps in the colon and rectum, some of which progress to

calenomatous polyps in the colon and rectum, some of which proragress to

calenomatous polyps in the colon and rectum, some of which proragress to

calenomatous polyps in the colon and rectum, some of which proragress to

calenomatous polyps in the colon and rectum, some of which proragress to

complement and the FAP locus is often found to be deleted in sporadic (i.e.,

colon-familial) adenomas and carcinomas, and chromosome 5q deletions have

also been observed in tumours of the lump, breast, colon, rectum,

chalder, liver, sarcomas, stomach, and prostate, and in leukaemias and

colon-familial adenomas stomach, and prostate, and in leukaemias and

colon-familial adversion to the prognosing or prognosing or prognosing or prognosing or prognosing or prognosing or prognosing or prognosing or prognosing or prognosing or prognosing neoplastic tissue,

conatic alteration of wild-type APC genes, and for testing therapeutic

detecting a genetic predisposition to cancer, for detecting germine and

contact alteration of wild-type APC genes, and for testing therapeutic

capants for the ability to suppress tumours. The present sequence

cerpresents a 2843 amino acid splice variant of the human APC protein.

This variant is more abundant than the 2742 amino acid variant (AAB23012) 120 120 240 300 300 360 360 420 HGNDKDSVLLGNSKGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC 420 09 9 Detecting Adenomatous Polypopsis Coli (APC) protein in a sample for diagnosing cancers, involves contacting the sample with antibodies that specifically bind to APC protein and detecting the complex formed. 61 ASSGQIDLIERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSRSGECSPVPMGSFPR 1 MAAASYDQLLKQVBALKMENSNLRQELBDNSNHLTKLBTBASNMKEVLKQLQGSIBDBAM 61 ASSGQIDLLERLKELNLDSSNFPGVKLRSKMSLRSYGSREGSVSSRSGECSPVPMGSFPR 181 QIDMIRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEKDILRIRQLLQSQAT BAERSSQNKHETGSHDAERQNEGGGVGEINWATSGNGQGSTTRMDHETASVLSSSSTHSA EAERSSQNKHETGSHDAERQNEGQGVGEINMATSGNGGGSTTRMDHETASVLSSSSTHSA PRRLISHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL PRRITSHLGTKVEMVYSLLSMLGTHDKDDMSRTLLAMSSSQDSCISMRQSGCLPLLIQLL 1 MAAASYDQLLKQVEALKMENSNLRQELEDNSNHLTKLETEASNMKEVLKQLQGSIEDEAM RGFVNGSRESTGYLEELEKERSLILLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEXDILRIRQLLQSQAT HGNDKDSVLLGNSRGSKEARARASAALHNIIHSQPDDKRGRREIRVLHLLEQIRAYCETC Gaps Length 2843; ; 0 0; Indels DB 3; Query Match
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2843; Conservative 0; Mismatches Claim 1; Fig 3A-C; 125pp; English Sequence 2843 AA; 121 121 181 241 241 301 301 361 361 ###X#X#DDDDDDDDDDDDDDDDDDDDDDDDXX à g ò .. d à g ò d පු පු 8 8 g ò

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VDCEMYGLINDHYSITLRRYAGMALINLIFGDVANKATLCSMKGCMRALVAQLKSESEDL

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WEWQEAHEPGMDQDKNPPMPAPVEHQICPAVCVIMKLSFDEEHRHAMNELGGLQAIAELLQ

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Kinzler K, Markham AF, Anand I 1 A, Nakamura Y, Vogelstein B;

Joslyn G, Kinz , Thliveris A,

Groden J, J White RL,

Carlson M, Gr Albertsen H, Hedge PJ;

WPI; 2000-565003/52. N-PSDB; AAA93449.

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                                                                                  QTDMTRRQLEYEARQIRVAMEEQLGTCQDMEKRAQRRIARIQQIEXDILRIRQLLQSQAT
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                      RGFVNGSRESTGYLEELEKERSLLLADLDKEEKEKDWYYAQLQNLTKRIDSLPLTENFSL
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developmental abnormality, anticancer drug, beta-catenin,
Wnt/Wg signalling pathway.
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This sequence represents a human APC protein which is used in a method of identifying candidate drugs for use in familial adenomatous polyposis (FAP) patients, or patients with increased risk of developing cancer. The protein can also be used to determine the presence or absence in a cell of wild type adenomatous polyposis coli (APC) gene or a downstream protein in the APC transcription regulatory pathway. This method involves introducing a Tcf-responsive reporter gene into the cell, and measuring transcription of the reporter gene does not have wild type APC or a downstream protein of the APC transcription regulatory pathway. The construction of the APC transcription regulatory pathway. The construction of the APC transcription regulatory pathway. The construction of the APC transcription regulatory pathway. The construction of being neoplastic and for treating a patient with colorectal cancer or other cancers associated with FAP, comprising administering to the patient a polypeptide comprising a portion of the APC sequence, comprising the beta-catenin binding site Disclosure; Page 32-37; 58pp; English.

Sequence 2973 AA;

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Matches 2843; Conservative 0; Mismatches 61 61 121 121 181 241 301 361 181 241 301 361 421 481 481 541 541 601 601 661 Dp g

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                                                    SLSSLDFDDDDVDLSREKAELRKAKENKESEAKVTSHTELTSNQQSANKTQAIAKQPINR
                                                                     GOPKPILOKOSTFPOSSKDIPDRGAATDEKLONFAIENTPVCFSHNSSLSSLSDIDQENN
                                                                                                                                                               NKENEPIKETEPPDSQGEPSKPQASGYAPKSFHVEDTPVCFSRNSSLSSLSIDSEDDLLQ
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The present sequence is a transcriptional activation protein related to the invention. The invention relates to human Tcf-4 proteins and their corresponding cDNA molecules which encodes transcriptional activation of factors of human Tcf/Lef family. Human Tcf-4 binds to beta-catenin and activates transcription in colorecal epithelial cells. Moreover it has been found that adenomatus polyposis coli (APC) regulates this conscriptional activation, by binding to beta-catenin. The invention also provides a recombinant adenovirus, Ad-Mini-Me ie., APC Minus its amino- and carboxyl -terminal Ends which expresses a fusion protein, cypen fluorescent protein (GPP)/CAPC containing GFP fused to the central cyphich contains its beta-catenin binding domain useful for third of APC which contains its beta-catenin binding domain useful for treating calcaer, e.g. colorectal cancer, and other cancers associated with Familial Adenomatous Polyposis (FAP) or patients with increased risk of developing cancer. Human Tcf-4 cDNA provides an excellent system for screening agents for their ability to promote cellivery, integration, hybridization, expression, replication or integration in cells or in a nample suspected of being neoplastic
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                                                                                                                                              Human, Tcf-4 protein; transcriptional activation factor; beta-catenin; apoptosis; colorectal cancer; Familial Adenomatous Polyposis; FAP; APC; adenomatous polyposis coli; recombinant adenovirus; Ad-Mini-Me; therapy; GFP; green fluorescent protein; GFP/CAPC fusion protein; cytostatic.
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                                                                                                         Transcriptional activation protein #1 related to the invention.
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standard; protein; 2973 AA
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Adenomatous polyposis coli; APC; transcriptional activation;
For responsive reporter gene, APC transcription regulatory pathway;
familial adenomatous polyposis; FAP; cancer; colorectal; thyroid; brain;
medulloblastoma; breast; head; neck; desmoid tumour; osteoma; cytostatic.
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                   2461 SFESLSPSSRPASPTRSQAQTPVLSPSLPDMSLSTHSSVQAGGWRKLPPNLSPTIEYNDG
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                                   The present sequence is a protein involved in cancer diagnosis associated with APC or beta-catenin mutations. Human Tcf-4E protein expressed in colorectal epithelium transactivates transcription when associated with beta-catenin. Adenomatous polyposis coli (APC) regulates this transcriptional activation, at least in part by binding to beta-catenin. Determining wild-type APC protein for diagnosing cancer comprises introducing a Tcf responsive reporter gene having upstream sequences of a Tcf responsive reporter gene having upstream sequences of a Tcf into a cell and measuring transcription of the reporter gene. The candidate drug identified is useful for treating familial adenomatous polyposis patients with APC or beta-catenin mutations and patients with increased risk of developing cancers such as colorectal, thyroid, brain, medulloblastoma, desmoid tumour, osteoma, breast, head and neck
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100.0%; Score 14559;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2842; Conservative 0; Mismatches
Disclosure; Page 58-65; 70pp; English.
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